

From: Gibbs, Terra  
Sent: Monday, January 06, 2003 10:50 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request...

) Could you please a regular search SEQ ID NO. 3

of Serial No. 10003354?

2) Also, please do an oligomer search of SEQ ID NO:3. Please limit the hits to 100 nucleotides or less.

**Terra Gibbs #79523**  
**AU 1635**  
**Mailbox 11E12**  
**306-3221**

THANK YOU!

Point of Contact:  
Barb O'Bryen  
Technical Information Specialist  
STIC CM1 6A05 308-4291

Searcher: BOB  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 1-13-03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (SEE 19)**

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 02:33:22 ; Search time 119 Seconds  
(without alignments)  
9568.830 Million cell updates/sec

Title: US-10-003-354-3  
Perfect score: 3713  
Sequence: 1 attaacaggccggttagg.....aaacttaagagttatta 3713

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 687286  
Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

- Database :
- 1: Issued Patents NA.\*
  - 2: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
  - 7: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17	0.5	42	4	US-09-171-425-2
C 2	17	0.5	48	4	US-09-171-425-6
C 3	17	0.5	48	4	US-09-171-425-7
C 4	17	0.5	54	1	US-08-390-850-1044
C 5	17	0.5	54	1	US-08-435-634-1044
C 6	16	0.4	49	6	5516641-1
C 7	16	0.4	87	4	US-09-364-543-84
C 8	16	0.4	97	1	US-08-182-175A-48
C 9	16	0.4	97	1	US-08-474-633A-57
C 10	16	0.4	97	4	US-08-823-771-57
C 11	16	0.4	97	5	PCT-US92-06412-48
C 12	15	0.4	18	2	US-08-890-980-64
C 13	15	0.4	18	3	US-08-890-979-64
C 14	15	0.4	18	3	US-09-032-894-64
C 15	15	0.4	18	4	US-09-031-626-64
C 16	15	0.4	19	2	US-08-656-906-3
C 17	15	0.4	19	4	US-09-217-847-3
C 18	15	0.4	21	3	US-08-851-350-23
C 19	15	0.4	21	3	US-08-851-350-33
C 20	15	0.4	22	1	US-08-379-078-64
C 21	15	0.4	22	4	US-07-974-409C-272
C 22	15	0.4	22	5	PCT-US93-00977-272
C 23	15	0.4	32	4	US-09-150-766-8
C 24	15	0.4	36	1	US-08-311-486C-424
C 25	15	0.4	36	3	US-08-582-740-5
C 26	15	0.4	36	4	US-09-109-879-5
C 27	15	0.4	44	2	US-08-700-670A-59

28	15	0.4	45	1	US-08-171-389-257	Sequence 257, App
29	15	0.4	45	1	US-08-123-936-257	Sequence 257, App
30	15	0.4	45	2	US-08-475-228A-257	Sequence 257, App
31	15	0.4	45	3	US-08-482-080A-257	Sequence 257, App
32	15	0.4	45	4	US-09-354-947-257	Sequence 257, App
33	15	0.4	45	5	PCT-US93-12388-257	Sequence 257, App
34	15	0.4	46	1	US-08-171-389-102	Sequence 102, App
35	15	0.4	46	1	US-08-123-936-102	Sequence 102, App
36	15	0.4	46	2	US-08-475-228A-102	Sequence 102, App
37	15	0.4	46	3	US-08-482-080A-102	Sequence 102, App
38	15	0.4	46	4	US-09-354-947-102	Sequence 102, App
39	15	0.4	46	5	PCT-US93-12388-102	Sequence 102, App
40	15	0.4	47	4	US-09-641-638-985	Sequence 985, App
C 41	15	0.4	56	4	US-09-390-867A-45	Sequence 45, Appl
C 42	15	0.4	56	4	US-09-390-867A-45	Sequence 45, Appl
C 43	15	0.4	56	4	US-09-548-260-45	Sequence 46, Appl
C 44	15	0.4	56	4	US-09-548-260-46	Sequence 46, Appl
45	15	0.4	74	3	US-08-812-121-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-171-425-2/c  
; Sequence 2, Application US/09171425A  
; Patent No. 6465438  
; GENERAL INFORMATION:  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Baker, Henry J.  
; APPLICANT: Smith, Bruce F.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
; FILE REFERENCE: 08909/003001  
; CURRENT APPLICATION NUMBER: US/09/171,425A  
; CURRENT FILING DATE: 1998-10-19  
; EARLIER APPLICATION NUMBER: PCT/EP97/01943  
; EARLIER FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 42  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotides  
US-09-171-425-2

Query Match 0.5% Score 17; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTTCTTCTT 2578  
Db 41 CCAGCTTCTTCTTCTT 25

RESULT 2  
US-09-171-425-6/c  
; Sequence 6, Application US/09171425A  
; Patent No. 6465438  
; GENERAL INFORMATION:  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Baker, Henry J.  
; APPLICANT: Smith, Bruce F.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
; FILE REFERENCE: 08909/003001  
; CURRENT APPLICATION NUMBER: US/09/171,425A  
; CURRENT FILING DATE: 1998-10-19  
; EARLIER APPLICATION NUMBER: PCT/EP97/01943  
; EARLIER FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6

; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotides  
US-09-171-425-6

Query Match 0.5%; Score 17; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCTT 2578  
|||||

Db 47 CCAGCTTCTCTCTCTT 31

## RESULT 3

US-09-171-425-7  
; Sequence 7, Application US/09171425A  
; Patent No. 6465438  
; GENERAL INFORMATION:  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Baker, Henry J.  
; APPLICANT: Smith, Bruce F.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
; FILE REFERENCE: 08909/003001  
; CURRENT APPLICATION NUMBER: US/09/171,425A  
; CURRENT FILING DATE: 1998-10-19  
; EARLIER APPLICATION NUMBER: PCT/EP97/01943  
; EARLIER FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotides  
US-09-171-425-7

Query Match 0.5%; Score 17; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2562 CCAGCTTCTCTCTCTT 2578  
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Db 6 CCAGCTTCTCTCTCTT 22

## RESULT 4

US-08-390-850-1044  
; Sequence 1044, Application US/08390850  
; Patent No. 5612215  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,850  
FILING DATE: February 17, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/354,920  
FILING DATE: December 13, 1994  
APPLICATION NUMBER: 08/152,487  
FILING DATE: No. 5612215ember 12, 1993  
APPLICATION NUMBER: 07/989,848  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1044:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-390-850-1044

Query Match 0.5%; Score 17; DB 1; Length 54;  
Best Local Similarity 94.1%; Pred. No. 1.3e+02;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3286 TCAGGGGAAGAGGGG 3302  
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Db 1 UCAGGGGAAGAGGGG 17

## RESULT 5

US-08-435-634-1044  
; Sequence 1044, Application US/08435634  
; Patent No. 5731295  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,634  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,850  
FILING DATE: February 17, 1995  
APPLICATION NUMBER: 08/354,920

;; FILING DATE: December 13, 1994  
;; APPLICATION NUMBER: 08/152,487  
;; FILING DATE: No. 5731295ember 12, 1993  
;; APPLICATION NUMBER: 07/989,848  
;; FILING DATE: December 7, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 211/084  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 1044:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 54 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-435-634-1044

Query Match 0.4%; Score 17; DB 1; Length 54;  
Best Local Similarity 94.1%; Pred. No. 1.3e+02;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3286 TCAGGGGAAGAGGGGG 3302  
Db 1 UCAGGGGAAGAGGGGG 17  
:|||||

RESULT 6  
5516641-1  
;; Patent No. 5516641  
;; APPLICANT: ULLMAN, EDWIN F.; GOODMAN, THOMAS C.;  
;; STULL, PAUL D.  
;; TITLE OF INVENTION: METHOD FOR DETECTION OF SPECIFIC  
;; NUCLEIC ACID SEQUENCES  
;; NUMBER OF SEQUENCES: 4  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 10-MAR-1995  
;; APPLICATION NUMBER: US/08/401,660  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 200,373  
;; FILING DATE: 18-FEB-1994  
;; APPLICATION NUMBER: 993,156  
;; FILING DATE: 18-DEC-1992  
;; APPLICATION NUMBER: 236,967  
;; FILING DATE: 25-AUG-1988  
;; SEQ ID NO: 1:  
;; LENGTH: 49  
5516641-1

Query Match 0.4%; Score 16; DB 6; Length 49;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2571 TTCTCTCTTTTCTTTT 2586  
Db 22 TTCTCTCTTTTCTTTT 37  
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RESULT 7  
US-09-364-543-84  
;; Sequence 84, Application US/09364543B  
;; Patent No. 6331394  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruckman, Judy  
;; APPLICANT: Gold, Larry  
;; APPLICANT: Stephens, Andrew  
;; APPLICANT: Janjic, Nebojsa  
;; TITLE OF INVENTION: Nucleic Acid Ligands to Integrins  
;; FILE REFERENCE: NEX82  
;; CURRENT APPLICATION NUMBER: US/09/364,543B

;; CURRENT FILING DATE: 1999-07-29  
;; NUMBER OF SEQ ID NOS: 118  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 84  
;; LENGTH: 87  
;; TYPE: RNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Sequence  
;; FEATURE:  
;; NAME/KEY: modified\_base  
;; LOCATION: (1)..(87)  
;; OTHER INFORMATION: All pyrimidines are 2' F.  
US-09-364-543-84

Query Match 0.4%; Score 16; DB 4; Length 87;  
Best Local Similarity 75.0%; Pred. No. 4.2e+02;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3350 ATCCACCCCTGCTTG 3365  
Db 23 AUCCACCCUGCCUUG 38  
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RESULT 8  
US-08-182-175A-48/c  
;; Sequence 48, Application US/08182175A  
;; Patent No. 5559223  
;; GENERAL INFORMATION:  
;; APPLICANT: Saverio Carl Falco  
;; APPLICANT: Sharon J. Keeler  
;; APPLICANT: Janet A. Rice  
;; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin  
;; NUMBER OF SEQUENCES: 113  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: E.I. du Pont de Nemours and Company  
;; STREET: 1007 Market Street  
;; CITY: Wilmington  
;; STATE: Delaware  
;; COUNTRY: USA  
;; ZIP: 19898  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy Disk  
;; COMPUTER: Macintosh  
;; OPERATING SYSTEM: Macintosh System, 6.0  
;; SOFTWARE: Microsoft Word, 4.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/182,175A  
;; FILING DATE:  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/743,006  
;; FILING DATE: 9 August 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Linda Axamethy Floyd  
;; REGISTRATION NUMBER: 33,692  
;; REFERENCE/DOCKET NUMBER: BB-1031  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (302) 992-4929  
;; TELEFAX: (302) 892-7949  
;; TELEX: 835420  
;; INFORMATION FOR SEQ ID NO: 48:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 97 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; ORIGINAL SOURCE:  
;; STRAIN: E. coli  
;; CELL TYPE: DH5 alpha  
;; IMMEDIATE SOURCE:

; CLONE: 86-H23  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2..88  
; OTHER INFORMATION: /function= "synthetic storage protein"  
; OTHER INFORMATION: /product= "protein"  
; OTHER INFORMATION: /gene= "ssp"  
; OTHER INFORMATION: /standard\_name= "5.8.8.5"  
; US-08-182-175A-48

Query Match 0.4%; Score 16; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202  
Db 52 CTCCTCCATCTTCTTC 37

RESULT 9  
US-08-474-633A-57/C  
; Sequence 57, Application US/08474633A  
; Patent No. 5773691  
; GENERAL INFORMATION:  
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY  
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE INCREASING THE LYSINE AND THREONINE CONTENT  
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MICROSOFT WORD VERSION 2.0C  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,633A  
; FILING DATE:

CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DH5 alpha  
IMMEDIATE SOURCE:  
CLONE: 86-H23  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..88  
OTHER INFORMATION: /function= "synthetic

; OTHER INFORMATION: storage protein  
; OTHER INFORMATION: /product= "protein"  
; OTHER INFORMATION: /gene= "ssp"  
; OTHER INFORMATION: /standard\_name= "5.8.8.5"  
; US-08-474-633A-57

Query Match 0.4%; Score 16; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202  
Db 52 CTCCTCCATCTTCTTC 37

RESULT 10  
US-08-823-771-57/c  
; Sequence 57, Application US/08823771  
; Patent No. 6459019  
; GENERAL INFORMATION:  
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY  
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE INCREASING THE LYSINE AND THREONINE CONTENT  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MICROSOFT WORD VERSION 2.0C  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/823,771  
; FILING DATE: 24-Mar-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/474,633  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420

INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DH5 alpha  
IMMEDIATE SOURCE:  
CLONE: 86-H23  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..88  
OTHER INFORMATION: /function= "synthetic

/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.8.8.5"

SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-08-823-771-57

Query Match 0.4%; Score 16; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202  
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DB 52 CTCCTCCATCTTCTTC 37

## RESULT 11

PCT-US92-06412-48/c

; Sequence 48, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing H

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06412

; FILING DATE: 19920807

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 97 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; STRAIN: E. coli

; CELL TYPE: DH5 alpha

; IMMEDIATE SOURCE:

; CLONE: 86-H23

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 2...88

; OTHER INFORMATION: /function= "synthetic storage protein

; OTHER INFORMATION: /product= "protein"

; OTHER INFORMATION: /gene= "ssp"

; OTHER INFORMATION: /standard\_name= "5.8.8.5"

PCT-US92-06412-48

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Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 CTCCTCCATCTTCTTC 2202  
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DB 52 CTCCTCCATCTTCTTC 37

## RESULT 12

US-08-890-980-64

; Sequence 64, Application US/08890980

; Patent No. 5998141

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan L.

; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/890,980

; FILING DATE: 10-JUL-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Arnold, Beth E.

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MIA-005.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer"

US-08-890-980-64

Query Match 0.4%; Score 15; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2777 AGGCTGAAGGAATGA 2791  
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DB 4 AGGCTGAAGGAATGA 18

## RESULT 13

US-08-890-979-64

; Sequence 64, Application US/08890979

; Patent No. 6030778

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan L.

; APPLICANT: Ordovas, Jose M.

; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,979  
; FILING DATE: 10-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MIA-005.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
US-08-890-979-64

Query Match 0.4%; Score 15; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2777 AGGCTGAAGGAATGA 2791  
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Db 4 AGGCTGAAGGAATGA 18

## RESULT 14

US-09-032-894-64  
; Sequence 64, Application US/09032894  
; Patent No. 6130041  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: MIA-005.03  
; CURRENT APPLICATION NUMBER: US/09/032,894  
; CURRENT FILING DATE: 1998-02-27  
; EARLIER APPLICATION NUMBER: 08/890,980  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
US-09-032-894-64

Query Match 0.4%; Score 15; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2777 AGGCTGAAGGAATGA 2791  
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Db 4 AGGCTGAAGGAATGA 18

## RESULT 15

US-09-031-626-64  
; Sequence 64, Application US/09031626  
; Patent No. 6228581  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.

; APPLICANT: Ordovas, Jose M.  
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND  
; FILE REFERENCE: MIA-005.04  
; CURRENT APPLICATION NUMBER: US/09/031,626  
; CURRENT FILING DATE: 1998-02-27  
; EARLIER APPLICATION NUMBER: 08/890,979  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
US-09-031-626-64

Query Match 0.4%; Score 15; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2777 AGGCTGAAGGAATGA 2791  
|||||  
Db 4 AGGCTGAAGGAATGA 18

Search completed: January 11, 2003, 06:08:28  
Job time : 121 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:49:57 ; Search time 4886 Seconds  
(without alignments)  
12307.377 Million cell updates/sec

Title: US-10-003-354-3

Perfect score: 3713  
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Scoring table: OLIGO.NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database:

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: em\_estfun:\*  
15: em\_estom:\*  
16: gb\_gss:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_other:\*  
25: em\_gss\_pro:\*  
26: em\_gss\_rnd:\*  
27: em\_gss\_rnd:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 3	21	0.6	74	D18644 MDCS01705
C 4	20	0.5	93	AM432832 SHB1F01.Y
C 5	20	0.5	99	AZ451477 1M0250D23
C 6	19	0.5	31	AZ579477 1M0367A08

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C <td>10<td>18<td>0.5<td>31<td>9</td><td>A1207866</td><td>A1207866 an06c06.x</td></td></td></td></td>	10 <td>18<td>0.5<td>31<td>9</td><td>A1207866</td><td>A1207866 an06c06.x</td></td></td></td>	18 <td>0.5<td>31<td>9</td><td>A1207866</td><td>A1207866 an06c06.x</td></td></td>	0.5 <td>31<td>9</td><td>A1207866</td><td>A1207866 an06c06.x</td></td>	31 <td>9</td> <td>A1207866</td> <td>A1207866 an06c06.x</td>	9	A1207866	A1207866 an06c06.x
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C <td>12<td>18<td>0.5<td>67<td>12</td><td>BF017439</td><td>BF017439 ux73G11.x</td></td></td></td></td>	12 <td>18<td>0.5<td>67<td>12</td><td>BF017439</td><td>BF017439 ux73G11.x</td></td></td></td>	18 <td>0.5<td>67<td>12</td><td>BF017439</td><td>BF017439 ux73G11.x</td></td></td>	0.5 <td>67<td>12</td><td>BF017439</td><td>BF017439 ux73G11.x</td></td>	67 <td>12</td> <td>BF017439</td> <td>BF017439 ux73G11.x</td>	12	BF017439	BF017439 ux73G11.x
C <td>13<td>18<td>0.5<td>68<td>12</td><td>BG771352</td><td>BG771352 602719421</td></td></td></td></td>	13 <td>18<td>0.5<td>68<td>12</td><td>BG771352</td><td>BG771352 602719421</td></td></td></td>	18 <td>0.5<td>68<td>12</td><td>BG771352</td><td>BG771352 602719421</td></td></td>	0.5 <td>68<td>12</td><td>BG771352</td><td>BG771352 602719421</td></td>	68 <td>12</td> <td>BG771352</td> <td>BG771352 602719421</td>	12	BG771352	BG771352 602719421
C <td>14<td>18<td>0.5<td>72<td>13</td><td>B1260363</td><td>B1260363 602969412</td></td></td></td></td>	14 <td>18<td>0.5<td>72<td>13</td><td>B1260363</td><td>B1260363 602969412</td></td></td></td>	18 <td>0.5<td>72<td>13</td><td>B1260363</td><td>B1260363 602969412</td></td></td>	0.5 <td>72<td>13</td><td>B1260363</td><td>B1260363 602969412</td></td>	72 <td>13</td> <td>B1260363</td> <td>B1260363 602969412</td>	13	B1260363	B1260363 602969412
C <td>15<td>18<td>0.5<td>99<td>14</td><td>BQ100462</td><td>BQ100462 1109B02.x</td></td></td></td></td>	15 <td>18<td>0.5<td>99<td>14</td><td>BQ100462</td><td>BQ100462 1109B02.x</td></td></td></td>	18 <td>0.5<td>99<td>14</td><td>BQ100462</td><td>BQ100462 1109B02.x</td></td></td>	0.5 <td>99<td>14</td><td>BQ100462</td><td>BQ100462 1109B02.x</td></td>	99 <td>14</td> <td>BQ100462</td> <td>BQ100462 1109B02.x</td>	14	BQ100462	BQ100462 1109B02.x
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C <td>17<td>17<td>0.5<td>51<td>10</td><td>AM208717</td><td>AM208717 uc63B06.x</td></td></td></td></td>	17 <td>17<td>0.5<td>51<td>10</td><td>AM208717</td><td>AM208717 uc63B06.x</td></td></td></td>	17 <td>0.5<td>51<td>10</td><td>AM208717</td><td>AM208717 uc63B06.x</td></td></td>	0.5 <td>51<td>10</td><td>AM208717</td><td>AM208717 uc63B06.x</td></td>	51 <td>10</td> <td>AM208717</td> <td>AM208717 uc63B06.x</td>	10	AM208717	AM208717 uc63B06.x
C <td>18<td>17<td>0.5<td>57<td>13</td><td>B1968595</td><td>B1968595 1032B09.x</td></td></td></td></td>	18 <td>17<td>0.5<td>57<td>13</td><td>B1968595</td><td>B1968595 1032B09.x</td></td></td></td>	17 <td>0.5<td>57<td>13</td><td>B1968595</td><td>B1968595 1032B09.x</td></td></td>	0.5 <td>57<td>13</td><td>B1968595</td><td>B1968595 1032B09.x</td></td>	57 <td>13</td> <td>B1968595</td> <td>B1968595 1032B09.x</td>	13	B1968595	B1968595 1032B09.x
C <td>19<td>17<td>0.5<td>59<td>10</td><td>AV838185</td><td>AV838185 AV838185</td></td></td></td></td>	19 <td>17<td>0.5<td>59<td>10</td><td>AV838185</td><td>AV838185 AV838185</td></td></td></td>	17 <td>0.5<td>59<td>10</td><td>AV838185</td><td>AV838185 AV838185</td></td></td>	0.5 <td>59<td>10</td><td>AV838185</td><td>AV838185 AV838185</td></td>	59 <td>10</td> <td>AV838185</td> <td>AV838185 AV838185</td>	10	AV838185	AV838185 AV838185
C <td>20<td>17<td>0.5<td>60<td>12</td><td>BF942724</td><td>BF942724 EST-CD15N</td></td></td></td></td>	20 <td>17<td>0.5<td>60<td>12</td><td>BF942724</td><td>BF942724 EST-CD15N</td></td></td></td>	17 <td>0.5<td>60<td>12</td><td>BF942724</td><td>BF942724 EST-CD15N</td></td></td>	0.5 <td>60<td>12</td><td>BF942724</td><td>BF942724 EST-CD15N</td></td>	60 <td>12</td> <td>BF942724</td> <td>BF942724 EST-CD15N</td>	12	BF942724	BF942724 EST-CD15N
C <td>21<td>17<td>0.5<td>60<td>13</td><td>B1156882</td><td>B1156882 602921624</td></td></td></td></td>	21 <td>17<td>0.5<td>60<td>13</td><td>B1156882</td><td>B1156882 602921624</td></td></td></td>	17 <td>0.5<td>60<td>13</td><td>B1156882</td><td>B1156882 602921624</td></td></td>	0.5 <td>60<td>13</td><td>B1156882</td><td>B1156882 602921624</td></td>	60 <td>13</td> <td>B1156882</td> <td>B1156882 602921624</td>	13	B1156882	B1156882 602921624
C <td>22<td>17<td>0.5<td>62<td>10</td><td>AM683571</td><td>AM683571 NF016A06L</td></td></td></td></td>	22 <td>17<td>0.5<td>62<td>10</td><td>AM683571</td><td>AM683571 NF016A06L</td></td></td></td>	17 <td>0.5<td>62<td>10</td><td>AM683571</td><td>AM683571 NF016A06L</td></td></td>	0.5 <td>62<td>10</td><td>AM683571</td><td>AM683571 NF016A06L</td></td>	62 <td>10</td> <td>AM683571</td> <td>AM683571 NF016A06L</td>	10	AM683571	AM683571 NF016A06L
C <td>23<td>17<td>0.5<td>70<td>13</td><td>B1452105</td><td>B1452105 G105.A05</td></td></td></td></td>	23 <td>17<td>0.5<td>70<td>13</td><td>B1452105</td><td>B1452105 G105.A05</td></td></td></td>	17 <td>0.5<td>70<td>13</td><td>B1452105</td><td>B1452105 G105.A05</td></td></td>	0.5 <td>70<td>13</td><td>B1452105</td><td>B1452105 G105.A05</td></td>	70 <td>13</td> <td>B1452105</td> <td>B1452105 G105.A05</td>	13	B1452105	B1452105 G105.A05
C <td>24<td>17<td>0.5<td>71<td>9</td><td>AA422570</td><td>AA422570 v14g10.s</td></td></td></td></td>	24 <td>17<td>0.5<td>71<td>9</td><td>AA422570</td><td>AA422570 v14g10.s</td></td></td></td>	17 <td>0.5<td>71<td>9</td><td>AA422570</td><td>AA422570 v14g10.s</td></td></td>	0.5 <td>71<td>9</td><td>AA422570</td><td>AA422570 v14g10.s</td></td>	71 <td>9</td> <td>AA422570</td> <td>AA422570 v14g10.s</td>	9	AA422570	AA422570 v14g10.s
C <td>25<td>17<td>0.5<td>72<td>9</td><td>A1081712</td><td>A1081712 cw81d11.s</td></td></td></td></td>	25 <td>17<td>0.5<td>72<td>9</td><td>A1081712</td><td>A1081712 cw81d11.s</td></td></td></td>	17 <td>0.5<td>72<td>9</td><td>A1081712</td><td>A1081712 cw81d11.s</td></td></td>	0.5 <td>72<td>9</td><td>A1081712</td><td>A1081712 cw81d11.s</td></td>	72 <td>9</td> <td>A1081712</td> <td>A1081712 cw81d11.s</td>	9	A1081712	A1081712 cw81d11.s
C <td>26<td>17<td>0.5<td>80<td>12</td><td>BF149230</td><td>BF149230 11.1.Huma</td></td></td></td></td>	26 <td>17<td>0.5<td>80<td>12</td><td>BF149230</td><td>BF149230 11.1.Huma</td></td></td></td>	17 <td>0.5<td>80<td>12</td><td>BF149230</td><td>BF149230 11.1.Huma</td></td></td>	0.5 <td>80<td>12</td><td>BF149230</td><td>BF149230 11.1.Huma</td></td>	80 <td>12</td> <td>BF149230</td> <td>BF149230 11.1.Huma</td>	12	BF149230	BF149230 11.1.Huma
C <td>27<td>17<td>0.5<td>80<td>17</td><td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td></td></td>	27 <td>17<td>0.5<td>80<td>17</td><td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td></td>	17 <td>0.5<td>80<td>17</td><td>AZ366225</td><td>AZ366225 1M0115C15</td></td></td>	0.5 <td>80<td>17</td><td>AZ366225</td><td>AZ366225 1M0115C15</td></td>	80 <td>17</td> <td>AZ366225</td> <td>AZ366225 1M0115C15</td>	17	AZ366225	AZ366225 1M0115C15
C <td>28<td>17<td>0.5<td>81<td>12</td><td>BG361932</td><td>BG361932 gpb49e07.Y</td></td></td></td></td>	28 <td>17<td>0.5<td>81<td>12</td><td>BG361932</td><td>BG361932 gpb49e07.Y</td></td></td></td>	17 <td>0.5<td>81<td>12</td><td>BG361932</td><td>BG361932 gpb49e07.Y</td></td></td>	0.5 <td>81<td>12</td><td>BG361932</td><td>BG361932 gpb49e07.Y</td></td>	81 <td>12</td> <td>BG361932</td> <td>BG361932 gpb49e07.Y</td>	12	BG361932	BG361932 gpb49e07.Y
C <td>29<td>17<td>0.5<td>89<td>14</td><td>BM731721</td><td>BM731721 sa183c04.Y</td></td></td></td></td>	29 <td>17<td>0.5<td>89<td>14</td><td>BM731721</td><td>BM731721 sa183c04.Y</td></td></td></td>	17 <td>0.5<td>89<td>14</td><td>BM731721</td><td>BM731721 sa183c04.Y</td></td></td>	0.5 <td>89<td>14</td><td>BM731721</td><td>BM731721 sa183c04.Y</td></td>	89 <td>14</td> <td>BM731721</td> <td>BM731721 sa183c04.Y</td>	14	BM731721	BM731721 sa183c04.Y
C <td>30<td>17<td>0.5<td>93<td>9</td><td>AA948071</td><td>AA948071 ok22e10.s</td></td></td></td></td>	30 <td>17<td>0.5<td>93<td>9</td><td>AA948071</td><td>AA948071 ok22e10.s</td></td></td></td>	17 <td>0.5<td>93<td>9</td><td>AA948071</td><td>AA948071 ok22e10.s</td></td></td>	0.5 <td>93<td>9</td><td>AA948071</td><td>AA948071 ok22e10.s</td></td>	93 <td>9</td> <td>AA948071</td> <td>AA948071 ok22e10.s</td>	9	AA948071	AA948071 ok22e10.s
C <td>31<td>17<td>0.5<td>93<td>10</td><td>AM230397</td><td>AM230397 uc03B06.Y</td></td></td></td></td>	31 <td>17<td>0.5<td>93<td>10</td><td>AM230397</td><td>AM230397 uc03B06.Y</td></td></td></td>	17 <td>0.5<td>93<td>10</td><td>AM230397</td><td>AM230397 uc03B06.Y</td></td></td>	0.5 <td>93<td>10</td><td>AM230397</td><td>AM230397 uc03B06.Y</td></td>	93 <td>10</td> <td>AM230397</td> <td>AM230397 uc03B06.Y</td>	10	AM230397	AM230397 uc03B06.Y
C <td>32<td>17<td>0.5<td>99<td>9</td><td>AA257812</td><td>AA257812 MBL2S3JG1</td></td></td></td></td>	32 <td>17<td>0.5<td>99<td>9</td><td>AA257812</td><td>AA257812 MBL2S3JG1</td></td></td></td>	17 <td>0.5<td>99<td>9</td><td>AA257812</td><td>AA257812 MBL2S3JG1</td></td></td>	0.5 <td>99<td>9</td><td>AA257812</td><td>AA257812 MBL2S3JG1</td></td>	99 <td>9</td> <td>AA257812</td> <td>AA257812 MBL2S3JG1</td>	9	AA257812	AA257812 MBL2S3JG1
C <td>33<td>16<td>0.4<td>19<td>17</td><td>A2941399</td><td>A2941399 2M0201F07</td></td></td></td></td>	33 <td>16<td>0.4<td>19<td>17</td><td>A2941399</td><td>A2941399 2M0201F07</td></td></td></td>	16 <td>0.4<td>19<td>17</td><td>A2941399</td><td>A2941399 2M0201F07</td></td></td>	0.4 <td>19<td>17</td><td>A2941399</td><td>A2941399 2M0201F07</td></td>	19 <td>17</td> <td>A2941399</td> <td>A2941399 2M0201F07</td>	17	A2941399	A2941399 2M0201F07
C <td>34<td>16<td>0.4<td>26<td>13</td><td>BM658913</td><td>BM658913 106602768</td></td></td></td></td>	34 <td>16<td>0.4<td>26<td>13</td><td>BM658913</td><td>BM658913 106602768</td></td></td></td>	16 <td>0.4<td>26<td>13</td><td>BM658913</td><td>BM658913 106602768</td></td></td>	0.4 <td>26<td>13</td><td>BM658913</td><td>BM658913 106602768</td></td>	26 <td>13</td> <td>BM658913</td> <td>BM658913 106602768</td>	13	BM658913	BM658913 106602768
C <td>35<td>16<td>0.4<td>44<td>17</td><td>AL760205</td><td>AL760205 Arabidops</td></td></td></td></td>	35 <td>16<td>0.4<td>44<td>17</td><td>AL760205</td><td>AL760205 Arabidops</td></td></td></td>	16 <td>0.4<td>44<td>17</td><td>AL760205</td><td>AL760205 Arabidops</td></td></td>	0.4 <td>44<td>17</td><td>AL760205</td><td>AL760205 Arabidops</td></td>	44 <td>17</td> <td>AL760205</td> <td>AL760205 Arabidops</td>	17	AL760205	AL760205 Arabidops
C <td>36<td>16<td>0.4<td>48<td>17</td><td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td></td></td>	36 <td>16<td>0.4<td>48<td>17</td><td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td></td>	16 <td>0.4<td>48<td>17</td><td>AZ646970</td><td>AZ646970 1M0513D15</td></td></td>	0.4 <td>48<td>17</td><td>AZ646970</td><td>AZ646970 1M0513D15</td></td>	48 <td>17</td> <td>AZ646970</td> <td>AZ646970 1M0513D15</td>	17	AZ646970	AZ646970 1M0513D15
C <td>37<td>16<td>0.4<td>50<td>13</td><td>BJ060889</td><td>BJ060889 BJ060889</td></td></td></td></td>	37 <td>16<td>0.4<td>50<td>13</td><td>BJ060889</td><td>BJ060889 BJ060889</td></td></td></td>	16 <td>0.4<td>50<td>13</td><td>BJ060889</td><td>BJ060889 BJ060889</td></td></td>	0.4 <td>50<td>13</td><td>BJ060889</td><td>BJ060889 BJ060889</td></td>	50 <td>13</td> <td>BJ060889</td> <td>BJ060889 BJ060889</td>	13	BJ060889	BJ060889 BJ060889
C <td>38<td>16<td>0.4<td>50<td>17</td><td>AL759584</td><td>AL759584 Arabidops</td></td></td></td></td>	38 <td>16<td>0.4<td>50<td>17</td><td>AL759584</td><td>AL759584 Arabidops</td></td></td></td>	16 <td>0.4<td>50<td>17</td><td>AL759584</td><td>AL759584 Arabidops</td></td></td>	0.4 <td>50<td>17</td><td>AL759584</td><td>AL759584 Arabidops</td></td>	50 <td>17</td> <td>AL759584</td> <td>AL759584 Arabidops</td>	17	AL759584	AL759584 Arabidops
C <td>39<td>16<td>0.4<td>54<td>12</td><td>BG814572</td><td>BG814572 da168h11</td></td></td></td></td>	39 <td>16<td>0.4<td>54<td>12</td><td>BG814572</td><td>BG814572 da168h11</td></td></td></td>	16 <td>0.4<td>54<td>12</td><td>BG814572</td><td>BG814572 da168h11</td></td></td>	0.4 <td>54<td>12</td><td>BG814572</td><td>BG814572 da168h11</td></td>	54 <td>12</td> <td>BG814572</td> <td>BG814572 da168h11</td>	12	BG814572	BG814572 da168h11
C <td>40<td>16<td>0.4<td>54<td>14</td><td>BQ265726</td><td>BQ265726 NISC.Ff08</td></td></td></td></td>	40 <td>16<td>0.4<td>54<td>14</td><td>BQ265726</td><td>BQ265726 NISC.Ff08</td></td></td></td>	16 <td>0.4<td>54<td>14</td><td>BQ265726</td><td>BQ265726 NISC.Ff08</td></td></td>	0.4 <td>54<td>14</td><td>BQ265726</td><td>BQ265726 NISC.Ff08</td></td>	54 <td>14</td> <td>BQ265726</td> <td>BQ265726 NISC.Ff08</td>	14	BQ265726	BQ265726 NISC.Ff08
C <td>41<td>16<td>0.4<td>54<td>17</td><td>AL758583</td><td>AL758583 Arabidops</td></td></td></td></td>	41 <td>16<td>0.4<td>54<td>17</td><td>AL758583</td><td>AL758583 Arabidops</td></td></td></td>	16 <td>0.4<td>54<td>17</td><td>AL758583</td><td>AL758583 Arabidops</td></td></td>	0.4 <td>54<td>17</td><td>AL758583</td><td>AL758583 Arabidops</td></td>	54 <td>17</td> <td>AL758583</td> <td>AL758583 Arabidops</td>	17	AL758583	AL758583 Arabidops
C <td>42<td>16<td>0.4<td>57<td>13</td><td>B1493094</td><td>B1493094 d197f01.Y</td></td></td></td></td>	42 <td>16<td>0.4<td>57<td>13</td><td>B1493094</td><td>B1493094 d197f01.Y</td></td></td></td>	16 <td>0.4<td>57<td>13</td><td>B1493094</td><td>B1493094 d197f01.Y</td></td></td>	0.4 <td>57<td>13</td><td>B1493094</td><td>B1493094 d197f01.Y</td></td>	57 <td>13</td> <td>B1493094</td> <td>B1493094 d197f01.Y</td>	13	B1493094	B1493094 d197f01.Y
C <td>43<td>16<td>0.4<td>59<td>9</td><td>A1336716</td><td>A1336716 qw87f05.x</td></td></td></td></td>	43 <td>16<td>0.4<td>59<td>9</td><td>A1336716</td><td>A1336716 qw87f05.x</td></td></td></td>	16 <td>0.4<td>59<td>9</td><td>A1336716</td><td>A1336716 qw87f05.x</td></td></td>	0.4 <td>59<td>9</td><td>A1336716</td><td>A1336716 qw87f05.x</td></td>	59 <td>9</td> <td>A1336716</td> <td>A1336716 qw87f05.x</td>	9	A1336716	A1336716 qw87f05.x
C <td>44<td>16<td>0.4<td>60<td>14</td><td>BQ090810</td><td>BQ090810 ku20e06.Y</td></td></td></td></td>	44 <td>16<td>0.4<td>60<td>14</td><td>BQ090810</td><td>BQ090810 ku20e06.Y</td></td></td></td>	16 <td>0.4<td>60<td>14</td><td>BQ090810</td><td>BQ090810 ku20e06.Y</td></td></td>	0.4 <td>60<td>14</td><td>BQ090810</td><td>BQ090810 ku20e06.Y</td></td>	60 <td>14</td> <td>BQ090810</td> <td>BQ090810 ku20e06.Y</td>	14	BQ090810	BQ090810 ku20e06.Y
C <td>45<td>16<td>0.4<td>60<td>17</td><td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td></td></td>	45 <td>16<td>0.4<td>60<td>17</td><td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td></td>	16 <td>0.4<td>60<td>17</td><td>CNS03VZ1</td><td>AL263062 Tetradon</td></td></td>	0.4 <td>60<td>17</td><td>CNS03VZ1</td><td>AL263062 Tetradon</td></td>	60 <td>17</td> <td>CNS03VZ1</td> <td>AL263062 Tetradon</td>	17	CNS03VZ1	AL263062 Tetradon

#### ALIGNMENTS

RESULT 1  
LOCUS AA833564 96 bp mRNA linear EST 31-DEC-1998  
DEFINITION aJ45C12.s1 Soares\_testis\_NHT Homo sapiens CDNA clone 1393270 3',  
mRNA sequence.  
ACCESSION AA833564  
VERSION AA833564.1 GI:2907292

KEYWORDS  
SOURCE  
ORGANISM

human.  
Homo sapiens

REFERENCE

1 (bases 1 to 96)  
Mammalia; Eutheria; Primates; Carnivora; Euteleostomi;  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Contact: Robert Strausberg, Ph.D.

JOURNAL

Comment: cgapbs-remail.nih.gov

COMMENT

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing

by: Washington University Genome Sequencing Center

Clone distribution

by: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/BLNM at:

www.bld.lnlnl.gov/dbtp/image/image.html

Insert Length: 856

Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 55.

FEATURES  
source Location/Qualifiers  
1. 96  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="1393270"  
/clone\_lib="Soares\_testis\_NHR"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc. and primed with a Not I - oligo(dT) primer [5']  
TGTTCACATCTGAGTGGAGCGCCGCCAATTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonalido."

BASE COUNT 36 a 14 c 8 g 38 t  
ORIGIN

Query Match 2.4%; Score 89; DB 9; Length 96;  
Best Local Similarity 100.0%; Pred. No. 5.6e-29;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3625 TTGCTCTACTTGTGATGTTTCAGAAATGCAATATATAAAGTATATGCTT 3684  
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DB 96 TTGCTCTACTTGTGATGTTTCAGAAATGCAATATATAAAGTATATGCTT 37  
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QY 3685 TAATGTAATTAAGCTTAATGAGTTATTTA 373  
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DB 36 TAATGTAATTAAGCTTAATGAGTTATTTA 8  
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RESULT 2  
A2822704/c 91 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0096K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0096K08 F, DNA sequence.  
ACCESSION A2822704  
VERSION A2822704.1 GI:12992612  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 91)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weils,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: K column: 08  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 91.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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FEATURES  
source Location/Qualifiers  
1. 91  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="UUGC2M0096K08"

/clone\_lib="Mouse 10kb plasmid.UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 28 a 19 c 20 g 24 t  
ORIGIN

Query Match 0.6%; Score 23; DB 17; Length 91;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2577 TTTTCTTTCTGAAAAAGCAA 2599  
|||||  
DB 54 TTTTCTTTCTGAAAAAGCAA 32  
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RESULT 3  
D18644 74 bp mRNA linear EST 12-DEC-1995  
LOCUS  
DEFINITION MUSGS01705 Mouse 3'-directed Mus musculus domesticus cDNA clone  
md0279 3', mRNA sequence.  
ACCESSION D18644  
VERSION D18644.1 GI:1100613  
KEYWORDS EST.  
SOURCE western European house mouse.  
ORGANISM Mus musculus domesticus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 74)  
Kawamoto,S., Okubo,K., Yoshii,U., Katsuki,M. and Matsubara,K.  
Analysis of gene expression in mouse embryogenesis by 3'-directed  
cDNA sequencing  
Unpublished (1995)  
Contact: Kawamoto,S., Okubo,K., Yoshii,U., Katsuki,M. and Matsubara  
K.  
Institute for Cellular and Molecular Biology  
Osaka University  
3-1 Yamada-oka, Suita, Osaka 565, Japan.  
Location/Qualifiers  
1. 74  
/organism="Mus musculus domesticus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10092"  
/clone="md0279"  
/clone\_lib="Mouse 3'-directed"  
/issue\_type="decidual tissue (day 6.5-8.5 of gestation)"

BASE COUNT 20 a 14 c 17 g 22 t  
ORIGIN

Query Match 0.6%; Score 21; DB 14; Length 74;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3681 GTTTTAATGTAATTAAGCTTTA 3701  
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DB 38 GTTTAATGTAATAACTTTA 58

RESULT 4  
 AM432832/c  
 LOCUS 93 bp mRNA linear EST 03-DEC-2001  
 DEFINITION shb1f01.v1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-c1016-6578 5', mRNA sequence.  
 ACCESSION AM432832  
 VERSION AM432832.1 GI:6964139  
 KEYWORDS EST  
 SOURCE soybean.  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 93)  
 AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,  
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,  
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,  
 R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,  
 R., Waterston,R. and Wilson,R.  
 TITLE Public Soybean EST Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Shoemaker R/Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: Resgen, Invitrogen Corp, 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact via email: cgen@resgen.com  
 Seq primer: -40RP from GIBCO.

FEATURES  
 source  
 Location/Qualifiers  
 1..93  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1016-6578"  
 /clone\_1lb="Gm-c1016"  
 /tissue\_type="Immature flowers of field grown plants"  
 /lab\_host="X110-Gold"  
 /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:  
 XhoI. This cDNA library was constructed from mRNA isolated  
 from immature flowers of field grown plants. The cDNA  
 library was prepared using the Stratagene pBluescript II  
 XR library construction kit. Complementary DNA was  
 synthesized from mRNA using a primer consisting of a poly-  
 (dT) sequence with a XhoI restriction site. EcoRI adapters  
 were ligated to the blunt-ended cDNA fragments followed by  
 XhoI digestion. The cDNA fragments were directionally  
 cloned into the EcoRI-XhoI restriction site of the  
 pBluescript vector. The ligated cDNA fragments were  
 transformed into X110-Gold host cells. This library was  
 constructed by Dr. Randy Shoemaker and Dr. John  
 Erpelting."

BASE COUNT 29 a 13 c 15 g 36 t  
 ORIGIN

Query Match 0.5%; Score 20; DB 10; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1,1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2564 ACCTTCCTCTCTCTTTT 2583  
 |||||||||||||||||||  
 DB 20 ACCTTCCTCTCTCTTTT 1

LOCUS AZ451477 99 bp DNA linear GSS 04-OCT-2000  
 DEFINITION IM0250D23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0250D23 R, DNA sequence.  
 ACCESSION AZ451477  
 VERSION AZ451477.1 GI:10607318  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 99)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0250 row: D column: 23  
 Seq primer: CACACAGCAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 99.

FEATURES  
 source  
 Location/Qualifiers  
 1..99  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0250D23"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain X110-Gold, T1-resistant, F-"  
 /note="Vector: pMD22ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase, and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD22 (g11473211419b1AF139072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli X110-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 12 a 15 c 18 g 54 t  
 ORIGIN

Query Match 0.5%; Score 20; DB 17; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1,1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2566 CTTTCCTCTCTCTTTT 2585  
 |||||||||||||||||||  
 DB 23 CTTTCCTCTCTCTTTT 42

RESULT 5  
 AZ451477

RESULT 6  
 AZ579477/c

LOCUS	AZ579477	31 bp	DNA	linear	GENS 13-DEC-2000
DEFINITION	IM0367A08P	Mouse 10kb plasmid	U08C1M	library	Mus musculus genomic
ACCESSION	AZ579477				
VERSION	AZ579477.1	GI:11693906			
KEYWORDS	GSS.				
ORGANISM	house mouse.				
SOURCE	Mus musculus				
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 31) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weils,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weils University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0367 row: A column: 08 Seq primer: CGTGTAAACGACGCGCCAGT Class: plasmid ends High quality sequence stop: 31. Location/Qualifiers 1..31				

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="U08C1M0367A08"
/clone_1lb="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g11473211419b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor DNA was annealed to the
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	0.5%	Score 19	DB 17	Length 31
Best Local Similarity	100.0%	Pred. No.	4.1e+03	
Matches 19, Conservative	0	Mismatches	0	Indels 0; Gaps 0;

<b>Qy</b>	<b>2568</b>	TTCCTCCTCCCTTCTTTCTT	<b>2586</b>
<b>Db</b>	<b>27</b>	TTCCTCCTCCCTTCTTTCTT	<b>9</b>

RESULT 7  
AZ322055/c

LOCUS	AZ322055	75 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	IM0042L1R9 Mouse 10kb plasmid U05C1M library Mus musculus genomic clone U05C1M0042L1R, DNA sequence.				
ACCESSION	AZ322055				
VERSION	AZ322055.1	GI:10375410			
KEYWORDS	GSS,				
SOURCE	house mouse,				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 75) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0042 row: L column: 19 Seq primer: CACACAGCAACACAGCTATGACC Class: plasmid ends High quality sequence stop: 75. Location/Qualifiers 1..75				
FEATURES					
source					

BASE COUNT  
ORIGIN

46 a 9 c 15 g 5 t

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0042L19"
/clone_1lb="Mouse 10Kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F'-"
/notes="vector: PMD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/nares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g11473211419b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match	0.5%	Score 19	DB 17	Length 75
Best Local Similarity	100.0%	Pred. No.	3.4e+03	
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY 2568 TTTCTTTCTTTCTTTT 2586
      |||||
Db 69 TTTCTTTCTTTT 51
```

RESULT 8  
AI810694

LOCUS A1810694 80 bp mRNA linear EST 07-JUL-1999  
 DEFINITION tui9h09.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2251553 3' similar to contains element 11 repetitive element ;, mRNA sequence.  
 ACCESSION A1810694  
 VERSION A1810694.1 GI:5397260  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 80)  
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMW.ac:  
 www-bio.liml.gov/bdnp/image/image.html  
 Seq primer: -400p from G1DCO  
 High quality sequence stop: 68.  
 Location/Qualifiers  
 1..80  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2251553"  
 /clone\_1lb="NCI\_CGAP\_Pr28"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 3 a 7 c 2 g 68 t  
 ORIGIN  
 Query Match 0.5%; Score 19; DB 9; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2568 TTCTCTCTCTTTT 2586  
 DB 15 TTCTCTCTCTTTT 33  
 RESULT 9  
 T52721/c 99 bp mRNA linear EST 06-FEB-1995  
 LOCUS ya72h02.s1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:67251 3' similar to similar to gb:x57766\_nal STROMELYSIN-3  
 DEFINITION PRECURSOR (HUMAN), mRNA sequence.  
 ACCESSION T52721  
 VERSION T52721.1 GI:654581  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 99)  
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins

LOCUS A1207866 31 bp mRNA linear EST 19-OCT-1998  
 DEFINITION an06c06.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684810 3' similar to SW:YH4\_PARIE P15615 HYPOTHETICAL 47.2  
 ACCESSION A1207866  
 VERSION A1207866.1 GI:3769808  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 31)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Ma, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-NCI human EST Project  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 FEATURES  
 source  
 Location/Qualifiers  
 1..99  
 /organism="Homo sapiens"  
 /db\_xref="GDB:488916"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:67251"  
 /clone\_1lb="Stratagene placenta (#937225)"  
 /sex="male"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /note="Organ: placenta; Vector: pluescript SK-; Site: 1: EcorI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' CATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTT 3'."  
 BASE COUNT 41 a 14 c 16 g 24 t 4 others  
 ORIGIN  
 Query Match 0.5%; Score 19; DB 14; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2568 TTCTCTCTCTTTT 2586  
 DB 57 TTCTCTCTCTTTT 39  
 RESULT 10  
 A1207866 31 bp mRNA linear EST 19-OCT-1998  
 LOCUS A1207866  
 DEFINITION an06c06.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684810 3' similar to SW:YH4\_PARIE P15615 HYPOTHETICAL 47.2  
 ACCESSION A1207866  
 VERSION A1207866.1 GI:3769808  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 31)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Ma, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-NCI human EST Project  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

# FEATURES

## source

1. .31  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1684810"  
 /clone\_lib="Stratagene schizo brain S11"  
 /sex="male"  
 /tissue\_type="schizophrenic brain S-11 frontal lobe"  
 /dev\_stage="34 years old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Vector: Bluescript SK-, Site 1: EcoRI; Library  
 constructed from S-11 frontal lobe, male, 34 years old,  
 50% caucasian, 50% Aleutian. Schizophrenic suicide.  
 Random primed into EcoRI site of ZAP II Vector. Mass  
 excised. Custom library. Avg insert length 1.4kb.  
 Material obtained by Johnston N., Torrey, E.F., Yolken R.,  
 and the Stanley Neuropathology Consortium - Analysis of  
 RNAs from the Brains of Individuals with Psychiatric  
 Diseases (unpublished) Stanley Neurovirology Laboratory,  
 Johns Hopkins School of Medicine, Baltimore MD."

# BASE COUNT

1 a 6 c 0 g 24 t

# ORIGIN

Query Match 0.5%; Score 18; DB 9; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2571 TTCTTCTTTTCTTCT 2588

Db 7 TTCTTCTTTTCTTCT 24

RESULT 11  
 A1422042 37 bp mRNA linear EST 30-MAR-1999  
 LOCUS t575705.x1 NCI-CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2103344 3'  
 DEFINITION similar to WP:F02E11.2 CE09193; , mRNA sequence.  
 A1422042  
 ACCESSION A1422042.1 GI:4267973  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 37)  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-r@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 www-bio.llnl.gov/dbp/image/image.html

Trace considered overall poor quality  
 Insert Length: 638 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

# FEATURES

## source

Location/Qualifiers  
 1. .37  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2103344"  
 /clone\_lib="NCI-CGAP\_Brn23"  
 /tissue\_type="glioblastoma (pooled)"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TCTTCCACATCTGAAAGTGGAGCCGCCGATCTTTTCTTTTCTTTTCTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT73 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M. Fatima Bonaldo."

# BASE COUNT

0 a 7 c 4 g 26 t

# ORIGIN

Query Match 0.5%; Score 18; DB 9; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2571 TTCTTCTTTTCTTCT 2588

Db 14 TTCTTCTTTTCTTCT 31

RESULT 12  
 BF017439/c 67 bp mRNA linear EST 29-DEC-2000  
 LOCUS uX73c11.x1 McCarrey Eddy type B spermatogonia Mus musculus cDNA  
 DEFINITION clone IMAGE:3654164 3', mRNA sequence.  
 BF017439  
 ACCESSION BF017439.1 GI:10748771  
 VERSION EST.  
 KEYWORDS house mouse.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 67)  
 Mairra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
 , B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter  
 , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R., and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 Other\_ESTs: uX73c11.y1  
 Contact: Mairra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:416468  
 Seq primer: Primer name ambiguous.

FEATURES  
 source  
 Location/Qualifiers  
 1. .67  
 /organism="Mus musculus"  
 /strain="CD-1"  
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 /clone="IMAGE:3654164"  
 /clone\_lib="McCarrey Eddy type B spermatogonia"  
 /sex="male"  
 /tissue\_type="type B spermatogonia, pooled from multiple  
 mice"  
 /dev\_stage="8 day"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: testis; Vector: pluescript SK+ (Stratagene

```

); Site.1: XhoI; Site.2: EcoRI; cDNA oligo dt-primed
[5'-(GA)10-ACTAGTCTCGAGTTTCTTTT-3'] and directionally
cloned using 5' linkers 5'-AATTCGACGAC-3' and
5'-CTCGTCGCG-3'. Size selection of >400bp material gives
average insert size ranging from 1-2 kb. Library was mass
excised (from lambda-UniZAP-XR) and resulting
single-stranded phagemids were prepped and transformed
into DH10B. Library contains 96% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63417."

BASE COUNT      15 a      12 c      15 g      25 t
ORIGIN

Query Match      0.5%; Score 18; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2961 ACTTACCAATGATTTT 2978
|||||
Db 45 ACTTACCAATGATTTT 28

RESULT 13
LOCUS BG771352 68 bp mRNA linear EST 15-MAY-2001
DEFINITION 602719421F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4840012 5',
mRNA sequence.
ACCESSION BG771352
VERSION BG771352.1 GI:14082005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 68)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LCM1670 row: 1 column: 05
High quality sequence stop: 60.
Location/Qualifiers
1..68
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4840012"
/clone_1id="NIH_MGC_60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (TI phase-resistant)"
/Note="Organ: prostate; Vector: pBNR-LIB (Clontech);
Site_1: SfiI (ggcgagctcgcc); Site_2: SfiI (ggcgatattggc);
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTAAGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCCGCGGCGCATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC

```

```

BASE COUNT      35 a      15 c      5 g      13 t
ORIGIN

Query Match      0.5%; Score 18; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2577 TTTTTCGTAAGAAA 2594
|||||
Db 48 TTTTTCGTAAGAAA 31

RESULT 14
LOCUS B1260363 72 bp mRNA linear EST 17-JUL-2001
DEFINITION 602969412F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108786 5',
mRNA sequence.
ACCESSION B1260363
VERSION B1260363.1 GI:14818593
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 72)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LAM11263 row: h column: 03
High quality sequence stop: 72.
Location/Qualifiers
1..72
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5108786"
/clone_1id="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/Note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT      44 a      4 c      6 g      18 t
ORIGIN

Query Match      0.5%; Score 18; DB 13; Length 72;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2577 TTTTTCGTAAGAAA 2594
|||||
Db 47 TTTTTCGTAAGAAA 30

RESULT 15
LOCUS BQ100462 99 bp mRNA linear EST 10-APR-2002
DEFINITION 1109b02.x1 Melton Amplified Mouse E16 5 Pancreas 3 M16S1 A Mus
musculus cDNA clone IMAGE:5941178 3', mRNA sequence.
ACCESSION BQ100462
VERSION BQ100462.1 GI:20133446
KEYWORDS EST.
SOURCE house mouse.

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ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 99)

REFERENCE  
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas  
 ,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,  
 Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other\_ESets: 1109b02.y1

TITLE  
 JOURNAL  
 COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmeltone@hwp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center This clone is  
 available royalty-free through LBNL; please contact the IMAGE  
 consortium (info@image.llnl.gov) for further information  
 Seq primer: -400p from Gibco  
 High quality sequence stop: 84.  
 location/Qualifiers  
 1. .99  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5941178"  
 /clone\_lib="Melton Amplified Mouse E16 5 Pancreas 3 M16S1  
 A"  
 /sex="Both"  
 /tissue\_type="pancreas"  
 /dev\_stage="Embryonic day E16.5"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1; Site\_1: Not 1; Site\_2: Sal 1;  
 Library constructed using Superscript plasmid library kit  
 (Life Technologies). cDNA made by oligo-dT priming.  
 Size-selected by column fractionation; average insert size  
 0.97 kb. Amplified once on solid support. cDNA library  
 Preparation: Guolin Chen."

BASE COUNT 21 a 23 c 17 g 38 t

ORIGIN

Query Match 0.5%; Score 18; DB 14; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 9e+03;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2961 ACTTACCAATGAAATTTT 2978  
 ||||||||||||||||  
 DB 46 ACTTACCAATGAAATTTT 29

Search completed: January 11, 2003, 03:15:09  
 Job time : 4892 secs





APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
FILE REFERENCE: rpi 247/282  
CURRENT APPLICATION NUMBER: US/09/504,231A  
PRIOR FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 09/274,553  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3242  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2705  
LENGTH: 36  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec

Query Match 0.4%; Score 16; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 CCTCATCAGCCTTGAA 618  
Db 16 CCTCATCAGCCTTGAA 1

RESULT 3  
US-09-274-553D-2705/c  
Sequence 2705, Application US/09274553D  
Patent No. US2002008225A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: MCSwigen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
FILE REFERENCE: rpi 247/282  
CURRENT APPLICATION NUMBER: US/09/274,553D  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3148  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2705  
LENGTH: 36  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec

Query Match 0.4%; Score 16; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 CCTCATCAGCCTTGAA 618  
Db 16 CCTCATCAGCCTTGAA 1

RESULT 4  
US-10-024-997-84  
Sequence 84, Application US/10024997  
Patent No. US20020150536A1  
GENERAL INFORMATION:  
APPLICANT: Ruckman, Judy  
APPLICANT: Gold, Larry  
APPLICANT: Stephens, Andrew  
APPLICANT: Janjic, Nebojsa  
TITLE OF INVENTION: Nucleic Acid Ligands to Integrins  
FILE REFERENCE: NEX82  
CURRENT APPLICATION NUMBER: US/10/024,997  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 09/364,543  
PRIOR FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 84  
LENGTH: 87  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
NAME/KEY: modified\_base  
LOCATION: (1)-(87)  
OTHER INFORMATION: All pyrimidines are 2' F.

Query Match 0.4%; Score 16; DB 12; Length 87;  
Best Local Similarity 75.0%; Pred. No. 6.5e+02;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3350 ATCCACCTGCTTG 3365  
Db 23 ATCCACCTGCTTG 38

RESULT 5  
US-09-859-214-5  
Sequence 5, Application US/09859214  
Patent No. US2002010311A1  
GENERAL INFORMATION:  
APPLICANT: Schwender, Charles F.  
Shroff, Hitesh N.  
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED  
INTERACTIONS AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02421  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/859,214  
FILING DATE: 16-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/109,879  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/582,740  
FILING DATE: 04-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS95-12A2

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 36 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-859-214-5

Query Match      0.4%; Score 15; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1449 CCATGATCCATCC 1463
DB  11 CCATGATCCATCC 25

RESULT 6
US-09-205-658-320/c
; Sequence 320, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205, 658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857, 076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888, 534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-205-658-320

Query Match      0.4%; Score 15; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  339 CGAGAGAGAGAGAA 353
DB  36 CGAGAGAGAGAGAA 22

RESULT 7
US-09-756-095-71
; Sequence 71, Application US/09756095
; Patent No. US20020115207A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd G.
; APPLICANT: Garcia-Blanco, Mariano A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
; TITLE OF INVENTION: SPLICOSOME MEDIATED RNA TRANS-SPLICING
; FILE REFERENCE: A31304-B-A 072874.0134
; CURRENT APPLICATION NUMBER: US/09/756, 095
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/158, 863
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/133, 717
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/087, 233
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; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 08/766, 354
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: 60/008, 317
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Branch point, pyrimidine tract and acceptor splice
; OTHER INFORMATION: site of PTM
US-09-756-095-71

Query Match      0.4%; Score 15; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2572 TCTCTTTTTTTTTT 2586
DB  15 TCTCTTTTTTTTTT 29

RESULT 8
US-09-946-807-1323
; Sequence 1323, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorodottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946, 807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795, 668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515, 716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1323
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1323

Query Match      0.4%; Score 15; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  3628 CCTCTACTTTGTATT 3642
DB  12 CCTCTACTTTGTATT 26

RESULT 9
US-09-795-668-1323
; Sequence 1323, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorodottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795, 668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515, 716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1323
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1323

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 61;
Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3628 CCTCTACTTGTATT 3642
DB 12 CCTCTACTTGTATT 26

RESULT 10
US-09-795-686-1323
; Sequence 1323, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1323
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-1323

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 61;
Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3628 CCTCTACTTGTATT 3642
DB 12 CCTCTACTTGTATT 26

RESULT 11
US-10-076-248-13
; Sequence 13, Application US/10076248
; Publication No. US20020135580A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd
; APPLICANT: Garcia-Blanco, Mariano
; APPLICANT: Puttaraju, Madalah
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
; FILE REFERENCE: A31304B-A-F 069906.0105
; CURRENT APPLICATION NUMBER: US/10/076,248
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 09/941,492
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 09/838,858
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 09/756,096
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/158,863
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/133,717
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/087,233
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 08/766,354
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; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: 60/008,317
; PRIOR FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTM branch point, polypyrimidine tract and
; OTHER INFORMATION: acceptor splice site
US-10-076-248-13

Query Match
Best Local Similarity 100.0%; Score 15; DB 9; Length 62;
Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2572 TCCTCTCTTTTCTTTT 2586
DB 15 TCCTCTCTTTTCTTTT 29

RESULT 12
US-09-920-300A-1268/C
; Sequence 1268, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1268
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 53
; OTHER INFORMATION: n = A,T,C or G
US-09-920-300A-1268

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 73;
Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2602 AGCACACGACACACA 2616
DB 68 AGCACACGACACACA 54

RESULT 13
US-10-033-528-1268/C
; Sequence 1268, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1268
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 53
; OTHER INFORMATION: n = A,T,C or G
US-10-033-528-1268

Query Match          0.4%; Score 15; DB 12; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2602 AGCACACAGCACACA 2616
    |||||
Db 68 AGCACACAGCACACA 54

RESULT 14
US-09-864-761-31308/C
; Sequence 31308, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecolica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31308

; LENGTH: 75
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC018516.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.48
US-09-864-761-31308

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Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2568 TTCTCTCTCTTTT 2582
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Db 17 TTCTCTCTCTTTT 3

RESULT 15
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; Sequence 6583, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(13401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 6583
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098625H1
US-09-878-574-6583

Query Match          0.4%; Score 15; DB 10; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 53 TCTTCTCTGAGAGA 67

Search completed: January 11, 2003, 06:06:14
Job time : 154 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:51:27 ; Search time 717 Seconds  
(without alignments)  
11662.022 Million cell updates/sec

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Scoring table:  
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Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	1.6	60	ABNA1013	Human spliced tran
2	19	0.5	50	ABU01023	Human SNP Involvin
3	18	0.5	36	AAQ25486	Purine rich HUMINT
4	18	0.5	51	AAH40868	Human SNP flanking
5	18	0.5	60	ABNA1363	Human spliced tran
6	17	0.5	25	AAAC96031	HLA HLA-C gene PCR
7	17	0.5	33	AAH46165	Hexokinase protein
8	17	0.5	38	AAH40778	Primer for Hpv6a L
9	17	0.5	41	AAH46167	Hexokinase protein

10	17	0.5	41	22	AAH46168	Hexokinase protein
c 11	17	0.5	48	18	AAH88795	Feline parvoviral
c 12	17	0.5	51	22	AAH39316	Human SNP flanking
c 13	17	0.5	54	17	AAH64429	Human stromelysin
c 14	17	0.5	82	16	AAH29416	Human gene signatu
c 15	16	0.4	24	16	AAH41135	Human gene signatu
c 16	16	0.4	24	20	AAH79281	Sequence VI to con
c 17	16	0.4	24	20	AAH79283	Genetic HCV NS3 pr
c 18	16	0.4	25	21	AAH96111	16S rRNA gene PCR
c 19	16	0.4	25	21	AAH96228	16S rRNA gene PCR
c 20	16	0.4	26	22	AAH14655	Human voltage-gate
c 21	16	0.4	28	19	AAH09936	Human biallelic po
c 22	16	0.4	47	21	AAH67873	Human map-related
c 23	16	0.4	51	22	AAH32726	Human SNP oligonuc
c 24	16	0.4	51	22	AAH73745	Human silent SNP c
c 25	16	0.4	52	18	AAH76376	Staphylococcus aur
c 26	16	0.4	53	21	AAH18812	Human secreted pro
c 27	16	0.4	59	21	AAH23038	Human secreted pro
c 28	16	0.4	60	24	ABN36070	Human spliced tran
c 29	16	0.4	60	24	ABN37919	Human spliced tran
c 30	16	0.4	60	24	ABNA7890	Human spliced tran
c 31	16	0.4	64	19	AAH73253	C. utilis crti pri
c 32	16	0.4	65	24	ABN30103	Rat spliced transcr
c 33	16	0.4	66	19	AAH73251	C. utilis crti pri
c 34	16	0.4	73	20	AAH79285	HCV NS3 protease 1
c 35	16	0.4	74	20	AAH79282	Genetic HCV NS3 pr
c 36	16	0.4	74	20	AAH79286	HCV NS3 protease 1
c 37	16	0.4	74	20	AAH79287	HCV NS3 protease 1
c 38	16	0.4	87	22	AAH73723	HCV NS3 protease 1
c 39	16	0.4	87	24	ABK31633	Integrin alpha v b
c 40	16	0.4	95	21	AAH14899	Antisense strand n
c 41	16	0.4	97	14	AAH37275	SSP 5.8-5.8.5 clone
c 42	16	0.4	97	16	AAH94994	Synthetic storage
c 43	16	0.4	97	19	AAH35832	Synthetic lysine-r
c 44	16	0.4	97	20	AAH95529	Hammerhead ribozym
c 45	15	0.4	17	21	AAH03348	

#### ALIGNMENTS

```
RESULT 1
ABNA1013
ID ABNA1013 standard; DNA; 60 BP.
XX ABNA1013:
XX
XX
XX 15-JUL-2002 (first entry)
XX
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:13761.
DE Human: mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-1B01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX
XX 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI, 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX
```

PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes -  
XX  
PS Example 1; SEQ ID 13761; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridizing selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of  
CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition; to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN55589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 60 BP; 23 A; 15 C; 15 G; 7 T; 0 other;  
  
Query Match 1.6%; Score 60; DB 24; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.4e-19;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1130 AATATGACCTCAAGGCTCACTACAAAGCGGCGCTCCGAGAAAGCGAGAG 1189  
DB 1 AATATGACCTCAAGGCTCACTACAAAGCGGCGCTCCGAGAAAGCGAGAG 60  
  
RESULT 2  
ABLO1023  
ID ABL01023 standard; DNA; 50 BP.  
XX  
AC ABL01023;  
XX  
DT 05-MAR-2002 (first entry)  
XX  
DE Human SNP involving a gap oligonucleotide SEQ ID NO:1014.  
XX  
KM Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
KM autoimmune disease; inflammation; cancer; nervous system disease;  
KM infection; polymorphic protein; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200138586-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 22-NOV-2000; 2000WO-US32311.  
XX  
PR 24-NOV-1999; 99US-0167383.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI; 2001-355949/37.  
XX  
PT Isolated human nucleic acids comprising one or more single nucleotide

PT polymorphisms, useful for treating a subject suffering from a  
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a  
PT sequence polymorphism -  
XX  
PS Claim 1; Page 554; 674pp; English.  
XX  
CC ABLO0010 to ABL01104 represent human nucleic acid oligonucleotides  
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
CC to ABB56903 represent human peptides encoded by some of the SNP  
CC oligonucleotides. The sequences from the present invention can have  
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
CC and antibodies from the present invention can be used for treating a  
CC subject suffering from, at risk for, or suspected of, suffering from a  
CC pathology ascribed to the presence of a sequence polymorphism. The  
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
CC are also useful for determining which forms of a characterised  
CC polymorphism are present in individuals. The antibodies may be used in  
CC the detection, quantitation and/or cellular or tissue localisation of a  
CC polymorphic protein (e.g., for use in measuring levels of the  
CC polymorphic protein within appropriate physiological samples).  
XX  
SQ Sequence 50 BP; 1 A; 11 C; 2 G; 36 T; 0 other;  
  
Query Match 0.5%; Score 19; DB 23; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2567 TTCTCTCTCTCTTTT 2585  
DB 8 TTCTCTCTCTCTTTT 26  
  
RESULT 3  
AAQ25486/C  
ID AAQ25486 standard; DNA; 36 BP.  
XX  
AC AAQ25486;  
XX  
DT 07-DEC-1992 (first entry)  
XX  
DE Purine rich HDNINT02 target duplex sequence.  
XX  
KM Target; human leukocyte adhesion protein p150,95 alpha subunit  
KM gene; AIDS; triplex; HIV; hepatitis; malignancy; inflammation; ds.  
XX  
OS Synthetic.  
XX  
PN WO9209705-A.  
XX  
PD 11-JUN-1992.  
XX  
PF 25-NOV-1991; 91WO-US08811.  
XX  
PR 23-NOV-1990; 90US-0617907.  
PR 18-JAN-1991; 91US-0643382.  
PR 08-APR-1991; 91US-0683420.  
PR 17-APR-1991; 91US-0686544.  
PR 17-APR-1991; 91US-0686546.  
PR 17-APR-1991; 91US-0686547.  
PR 27-SEP-1991; 91US-0766733.  
XX  
PA (GILE-) GILEAD SCI INC.  
XX  
PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;  
XX  
DR WPI; 1992-217083/26.  
XX  
PT New oligomers contg. modified bases - which form a triplex with  
PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,  
PT hepatitis, herpes, malignancy and inflammation  
XX



PS Claim 11; Page 64; 77pp; English.

XX The sequence depicts a HUMINT02 sequence beginning at nucleotide  
CC 2370. The sequence is a viral duplex sequence which contains a  
CC putative-rich region concentrated on one chain of the duplex. The  
CC sequence may be prepred. by standard DNA synthesis. The HUMINT02  
CC duplex sequence is used as a target for novel oligomers which are  
CC capable of forming a triplex at physiological pH by coupling into  
CC the major groove of the DNA duplex. Two such oligomers LAP  
CC 321-2 are capable of forming a triplex with this sequence. The  
CC oligomers are used in the treatment of inflammation. Similar oligomers  
CC may be used to target viral DNA duplexes specific for HIV, herpes and  
CC other viruses. The triple helices form under mild conditions thus  
CC assays may be carried out without subjecting the test specimen to  
CC harsh conditions. The oligomer is able to inhibit gene expression,  
CC as verified by in vitro systems.  
CC See also AA025452-25501 and AA030226-448.

XX Sequence 36 BP; 27 A; 0 C; 9 G; 0 U; 0 other;

SQ

Query Match 0.5%; Score 18; DB 13; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2568 TTTCTCTCTCTTTT 2585  
|||||  
DB 18 TTTCTCTCTCTTTT 1

RESULT 4  
AAH40868  
ID AAH40868 standard; DNA; 51 BP.  
AC AAH40868;  
XX  
XX 14-AUG-2001 (first entry)  
DE Human SNP flanking oligonucleotide SEQ ID 3664.  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNEP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200129262-A2.  
PN  
XX 26-APR-2001.  
PD  
XX 13-OCT-2000; 2000WO-US28436.  
PF  
XX 15-OCT-1999; 9905-0160096.  
PR  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
PA  
XX Plcoult-Newburg L, Pohl M;  
PI  
XX WPI; 2001-290930/30.  
DR  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample  
XX  
XX Claim 1; Page 68; 83pp; English.

PS Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNEP) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a

CC SNP flanking sequence, the SNEP primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a fragment of human  
CC DNA flanking the site of a single nucleotide polymorphism.

XX Sequence 51 BP; 5 A; 15 C; 8 G; 23 T; 0 other;

SQ

Query Match 0.5%; Score 18; DB 22; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2567 TTTCTCTCTTTT 2584  
|||||  
DB 34 TTTCTCTCTTTT 51

RESULT 5  
ABN41363  
ID ABN41363 standard; DNA; 60 BP.  
XX  
XX ABN41363;  
AC  
XX 15-JUL-2002 (first entry)  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14111.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
KW  
XX Homo sapiens.  
OS  
XX WO200210449-A2.  
PN  
XX 07-FEB-2002.  
PD  
XX 20-JUL-2001; 2001WO-IB01903.  
PF  
XX 28-JUL-2000; 2000US-221607P.  
PR  
XX 02-MAY-2001; 2001US-287724P.  
PR  
XX (COMP-) COMPUGEN INC.  
PA  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
PI  
XX WPI; 2002-257383/30.  
DR  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of  
PT a genome, useful for detecting tissue-, pathology-, and  
PT developmental-specific genes  
XX  
XX Example 1; SEQ ID 14111; 47pp; English.

PS The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the  
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises  
CC several oligonucleotides, each capable of hybridising selectively to a  
CC set of messenger RNAs transcribed from a given transcription unit of

CC the genome, which encodes one or more messenger RNA splice variants.  
CC The oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterizing the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC particular biological or pathological state, and so allowing the  
CC detection of tissue- and pathology-specific genes such as those genes  
CC only expressed in specific tissue under a specific pathological  
CC condition: to detect developmental specific genes; and to detect RNA  
CC transcripts and splice variants of a transcriptome of a patient suffering  
CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 60 BP; 11 A; 21 C; 15 G; 13 T; 0 other;  
  
Query Match 0.5%; Score 18; DB 24; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2727 TGCCAGAGACAGCTCTC 2744  
18 TGCCAGAGACAGCTCTC 35  
Db  
  
RESULT 6  
AAC96031  
ID AAC96031 standard; DNA; 25 BP.  
AC AAC96031;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA HLA-C gene PCR primer #43.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PE 20-APR-2000; 2000WO-EP03636.  
XX  
PR 26-APR-1999; 99EP-0303215.  
XX  
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI: 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences  
PT of specific length -  
XX  
PS Claim 14; Page 44; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular.  
XX  
SQ Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 other;  
  
Query Match 0.5%; Score 17; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2999 TTTTGTGCTCTC 3015  
6 TTTTGTGCTCTCTC 22  
Db  
  
RESULT 7  
AAH46165  
ID AAH46165 standard; DNA; 33 BP.  
AC AAH46165;  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Hexokinase protein 12 PCR primer, SEQ ID NO:5.  
XX  
KW Hexokinase protein 12; human; recombinant production;  
KW malignant tumour; cancer; blood disease; HIV infection;  
KW human immunodeficiency virus; immune disorder; inflammatory condition;  
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147968-A1.  
XX  
PD 05-JUL-2001.  
XX  
PE 18-DEC-2000; 2000WO-CN00597.  
XX  
PR 23-DEC-1999; 99CN-0125723.  
XX  
PA (UYFU-) UNIV FUDAN.  
PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI: 2001-418227/44.  
XX  
PT Hexokinase protein 12 and encoded polynucleotide, applicable in  
PT diagnosis and treatment of cancer, hemopathy, HIV infection,  
PT immunological diseases and phlogosis -  
XX  
PS Example 5; Page 17; 35pp; Chinese.  
XX  
CC The invention relates to hexokinase protein 12 (AAH3785), nucleic acids  
CC encoding it (AAH46162), and a method for the recombinant production of  
CC hexokinase protein 12. The present invention additionally discloses an  
CC antagonist of hexokinase protein 12 for therapeutic use, and an antibody  
CC which specifically binds to hexokinase protein 12. Hexokinase protein 12,  
CC and nucleotides which encode it may be used for treating a variety of  
CC diseases, such as malignant tumours, blood diseases, HIV (human  
CC immunodeficiency virus) infection, immune disorders and inflammatory  
CC conditions. The protein may also be used to screen for modulators of its  
CC activity or for peptide fingerprinting identification. The polynucleotide  
CC can be used as a primer for nucleic acid amplification reactions or as a  
CC probe for hybridisation reactions, or in producing gene chips or  
CC microarrays. Sequences AAH46165-AAH46166 represent PCR primers used in  
CC an exemplification of the invention to amplify human hexokinase protein  
CC 12 cDNA for cloning.  
XX  
SQ Sequence 33 BP; 9 A; 6 C; 9 G; 9 T; 0 other;  
  
Query Match 0.5%; Score 17; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2692 CATGGTGTATGAGA 2708  
|||  
DB 16 CATGGTGTATGAGA 32

## RESULT 8

AAT40778/c  
ID AAT40778 standard; CDNA; 38 BP.

AC AAT40778;

DF 26-NOV-1996 (first entry)

DE primer for HPV6a L2 gene amplification.

KM MNN9; yeast; disrupt; human papilloma virus; capsid protein;  
KM prevent; vaccine; infection; treat; primer; PCR; probe; ss.

OS Synthetic.

PN MO9615247-A1.

XX 23-MAY-1996.

PE 13-NOV-1995; 95WO-US15027.

PR 14-NOV-1994; 94US-0339368.

PA (MERI) MERCK & CO INC.

PI Cook JC, George HA, Hofmann KJ, Jansen KU, Joyce JG;  
PI Lehman ED, Markushz, Schultz LD;

DR WPI: 1996-268219/27.

XX Papilloma: virus capsid proteins, pref. L1, L2, L1 + L2 and derivs.  
PT useful in vaccines to treat or prevent papillomavirus infection

PS Example 14; Page 30; 92pp; English.

CC AAT40774-78 are primers used in the cloning of human papilloma virus  
CC (HPV) strain 6a capsid protein genes L1, L2 and L1+L2. Yeast strains  
CC contg. disrupted genes (see AAT40768-73) were used for the isolation of  
CC HPV capsid proteins. The capsid proteins are useful in vaccines to treat  
CC or prevent HPV infection. The present sequence is a 3' antisense primer  
CC used to amplify the HPV6a L2 gene.

XX Sequence 38 BP; 12 A; 12 C; 9 G; 5 T; 0 other;

Query Match 0.5%; Score 17; DB 17; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 TTTTTCAGATGCGC 86  
|||  
DB 33 TTTTTCAGATGCGC 17

## RESULT 9

AAH46167

ID AAH46167 standard; DNA; 41 BP.

AC AAH46167;

DT 21-SEP-2001 (first entry)

DE Hexokinase protein 12 probe, SEQ ID NO:8.

KW Hexokinase protein 12; human; recombinant production;  
KW malignant tumor; cancer; blood disease; HIV infection;

KW human immunodeficiency virus; immune disorder; inflammatory condition;  
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

OS Homo sapiens.

PN WO200147968-A1.

XX 05-JUL-2001.

PE 18-DEC-2000; 2000WO-CN00597.

PR 23-DEC-1999; 99CN-0125723.

PA (YIFU-) UNIV FUDAN.

PI (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

DR Mao Y, Xie Y;

DR WPI: 2001-418227/44.

PT Hexokinase protein 12 and encoded polynucleotide, applicable in  
PT diagnosis and treatment of cancer, hemopathy, HIV infection,  
PT immunological diseases and phlogosis

PS Example 7; Page 20; 35pp; Chinese.

CC The invention relates to hexokinase protein 12 (AAB73785), nucleic acids  
CC encoding it (AAH46162), and a method for the recombinant production of  
CC hexokinase protein 12. The present invention additionally discloses an  
CC antagonist of hexokinase protein 12 for therapeutic use, and an antibody  
CC which specifically binds to hexokinase protein 12. Hexokinase protein 12,  
CC and nucleotides which encode it may be used for treating a variety of  
CC diseases, such as malignant tumours, blood diseases, HIV (human  
CC immunodeficiency virus) infection, immune disorders and inflammatory  
CC conditions. The protein may also be used to screen for modulators of its  
CC activity or for peptide fingerprinting identification. The polynucleotide  
CC can be used as a primer for nucleic acid amplification reactions or as a  
CC probe for hybridisation reactions, or in producing gene chips or  
CC microarrays. Sequences AAH46167-AAH46168 represent hexokinase protein 12  
CC probes used in an exemplification of the invention.

XX Sequence 41 BP; 7 A; 7 C; 12 G; 15 T; 0 other;

Query Match 0.5%; Score 17; DB 22; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2692 CATGGTGTATGAGA 2708  
|||  
DB 6 CATGGTGTATGAGA 22

## RESULT 10

AAH46168

ID AAH46168 standard; DNA; 41 BP.

AC AAH46168;

DT 21-SEP-2001 (first entry)

DE Hexokinase protein 12 probe, SEQ ID NO:9.

KW Hexokinase protein 12; human; recombinant production;  
KW malignant tumor; cancer; blood disease; HIV infection;

KW human immunodeficiency virus; immune disorder; inflammatory condition;  
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

OS Homo sapiens.

PN WO200147968-A1.

XX 05-JUL-2001.

PE 18-DEC-2000; 2000WO-CN00597.

PR 23-DEC-1999; 99CN-0125723.

XX (UYEU-) UNIV FUDAN.  
PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.  
XX Mao Y, Xie Y;  
PI WPI; 2001-418227/44.  
XX  
PT Hexokinase protein 12 and encoded polynucleotide, applicable in  
PT diagnosis and treatment of cancer, hemopathy, HIV infection,  
PT immunological diseases and phlogosis  
PS Example 7; Page 20; 35pp; Chinese.  
XX  
CC The invention relates to hexokinase protein 12 (AA873785), nucleic acids  
CC encoding it (AAH46162), and a method for the recombinant production of  
CC hexokinase protein 12. The present invention additionally discloses an  
CC antagonist of hexokinase protein 12 for therapeutic use, and an antibody  
CC which specifically binds to hexokinase protein 12. Hexokinase protein 12,  
CC and nucleotides which encode it may be used for treating a variety of  
CC diseases, such as malignant tumors, blood diseases, HIV (human  
CC immunodeficiency virus) infection, immune disorders and inflammatory  
CC conditions. The protein may also be used to screen for modulators of its  
CC activity or for peptide fingerprinting identification. The polynucleotide  
CC can be used as a primer for nucleic acid amplification reactions or as a  
CC probe for hybridisation reactions, or in producing gene chips or  
CC microarrays. Sequences AAH46167-AAH46168 represent hexokinase protein 12  
CC probes used in an exemplification of the invention.  
XX  
SQ Sequence 41 BP; 7 A; 6 C; 12 G; 16 T; 0 other;  
XX  
Query Match 0.5%; Score 17; DB 22; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2692 CATGGTGTATGAGA 2708  
DB 6 CATGGTGTATGAGA 22  
|||||  
RESULT 11  
AA8795/C  
ID AA8795 standard; DNA; 48 BP.  
XX  
AC AA8795;  
XX  
DT 24-APR-1998 (first entry)  
XX  
DE Feline parvoviral VP1 T cell epitope encoding DNA.  
XX  
DE Parvovirus; feline; canine; T cell epitope; VP1; VP2; vaccine;  
XX  
KW Immunogen; nucleocapsid protein; cat; dog; mink; ss.  
XX  
OS Synthetic.  
OS Parvovirus.  
XX  
FH Key Location/Qualifiers  
FT 7..48  
FT CDS /tag= a  
FT /note= "The stop codon is not indicated"  
FT  
XX  
XX WO9740163-A1.  
XX  
XX 30-OCT-1997.  
XX  
XX 18-APR-1997; 97WO-EP01943.  
XX  
XX 19-APR-1996; 96EP-0106217.  
XX  
XX (COLP/) COLPAN M.  
XX  
XX Baker HJ, Colpan M, Schorr J, Smith BF;  
XX  
XX

DR WPI; 1997-535847/49.  
DR P-PSDB; AAM31733.  
XX  
XX Vaccine containing nucleic acid expressing parvoviral epitope -  
PT particularly both B and T cell epitope(s), for immunisation of cats,  
PT dogs and mink against parvoviruses, also as a carrier for other  
PT antigens  
PS Claim 12; Page 15; 30pp; English.  
XX  
CC This synthetic nucleotide sequence encodes the T-cell epitope of a  
CC parvoviral VP1 nucleocapsid protein. This is used in the preparation of  
CC an anti-parvovirus vaccine. The anti-parvovirus vaccine contains nucleic  
CC acid encoding at least one parvovirus-specific VP1 or VP2 T/B cell  
CC antigenic epitope plus a carrier. The anti-parvovirus vaccine are  
CC especially used to protect cats, dogs and mink, e.g. against feline  
CC panleukopenia virus, mink enteritis virus or gastroenteritis caused by  
CC canine parvovirus (CPV). The vaccine also includes an adjuvant,  
CC particularly a DNA containing unmethylated CpG motifs i.e. ISO. The ISO  
CC contains phosphorothioate linkages and is a powerful immune activator.  
CC The vaccine may also be used to deliver other immunogens, e.g. (human)  
CC hepatitis B surface antigen. Immunisation with naked DNA provides good  
CC protection against parvovirus after only one injection. Both humoral and  
XX cellular responses may be induced.  
XX  
SQ Sequence 48 BP; 19 A; 11 C; 9 G; 9 T; 0 other;  
XX  
Query Match 0.5%; Score 17; DB 18; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2562 CCAGCTTCTCTCTCTCT 2578  
DB 47 CCAGCTTCTCTCTCTCT 31  
|||||  
RESULT 12  
AAH39316/C  
ID AAH39316 standard; DNA; 51 BP.  
XX  
AC AAH39316;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE Human SNP flanking oligonucleotide SEQ ID 2112.  
XX  
DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX  
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
XX  
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX  
XX inflammation; forensic investigation; paternity analysis; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200129262-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 13-OCT-2000; 2000WO-US28436.  
XX  
XX 15-OCT-1999; 99US-0160096.  
XX  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
XX Picoult-Newburg L, Pohl M;  
XX  
XX WPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
XX  
XX absence or identity of single polynucleotide polymorphism in a nucleic  
XX  
XX acid sample  
XX  
XX

PS Claim 1; Page 60; 83bp; English.

XX  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a fragment of human  
CC DNA flanking the site of a single nucleotide polymorphism.

XX  
SQ Sequence 51 BP; 20 A; 9 C; 7 G; 15 T; 0 other;

Query Match 0.5%; Score 17; DB 22; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2577 TTTTTCGCGAATA 2593  
|||||  
DB 19 TTTTTCGCGAATA 3

RESULT 13  
AAH64429  
ID AAH64429 standard; RNA; 54 BP.

AC AAH64429;  
XX  
DT 20-JUL-1999 (first entry)  
XX  
DE Human stromelysin hairpin ribozyme SEQ ID NO:1061.  
XX  
KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN MO9618736-A2.  
XX  
PD 20-JUN-1996.  
XX  
PF 22-NOV-1995; 95WO-0515516.  
XX  
XX 05-OCT-1995; 95US-0541365.  
PR 13-DEC-1994; 94US-0354920.  
PR 23-DEC-1994; 94US-0363253.  
PR 23-DEC-1994; 94US-0363258.  
PR 17-FEB-1995; 95US-0390850.  
PR 20-APR-1995; 95US-0426124.  
PR 02-MAY-1995; 95US-0432874.  
PR 04-MAY-1995; 95US-0434509.  
PR 07-JUL-1995; 95US-0000951.  
PR 07-JUL-1995; 95US-0000974.  
PR 07-AUG-1995; 95US-0512861.

XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;  
PI Beigelman L, Karpelsky A, Modak A, Usman N, Burgin A;  
PI Matlicic-Adamic J, Jarvis T, Thompson JD, Wincott F;  
XX  
XX WPI; 1996-300653/30.

XX  
XX Enzymatic nucleic acid molecules having a hammer-head motif - used  
PT for the treatment of arthritis, induction of graft tolerance or  
PT treatment of auto-immune diseases

XX  
PS Example 1; Page 164; 307bp; English.

XX  
XX The present invention describes a novel enzymatic nucleic acid (ENA)  
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose  
CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)  
CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.  
CC The ENA's can inhibit collagenase and stromelysin production in the  
CC synovial membrane of joints for the treatment or prevention of arthritis,  
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
CC be used to treat antigen presenting cells of a donor to induce tolerance  
CC in a recipient to an alloantigen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC stromelysin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment  
CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention.

XX  
SQ Sequence 54 BP; 18 A; 9 C; 18 G; 9 U; 0 other;

Query Match 0.5%; Score 17; DB 17; Length 54;  
Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3286 TCAGGGGAGAGAGGGCG 3302  
:|||||  
DB 1 DCAGGGGAGAGAGGGCG 17

RESULT 14  
AAT20416  
ID AAT20416 standard; CDNA to mRNA; 82 BP.  
XX  
AC AAT20416;  
XX  
DT 19-JUL-1996 (first entry)  
XX  
DE Human gene signature HDNGS01570.  
XX  
KW Gene signature: messenger RNA; mRNA; relative abundance; frequency;  
KW human; Cloning; mapping; non-biased library; diagnosis; detection;  
KW cell typing; abnormal cell function; ss.  
XX  
OS Homo sapiens.  
OS  
XX  
PN WO9514772-A1.  
XX  
PD 01-JUN-1995.  
XX  
PF 11-NOV-1994; 94WO-JP01916.  
XX  
PR 12-NOV-1993; 93JP-0355504.  
XX  
PA (MATS/) MATSUBARA K.  
PA (OKUBO/) OKUBO K.  
XX  
PI Matsubara K, Okubo K;

```

XX
XX WPI; 1995-206931/27.
XX
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
XX for diagnosis of abnormal cell function, by preparing cDNA that
XX reflects relative abundance of corresp. mRNA in specific human
XX tissues
XX
XX Claim 1; Page 632; 2245pp; Japanese.
XX
XX A single-stranded DNA (or its complementary strand or the corresp.
XX double-stranded DNA) which comprises one of the 7837 "GS" sequences
XX given in AAT19001-T26837 and which is able to hybridize to part of
XX human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
XX sequences were obtained from 3'-directed cDNA libraries prepared
XX from various human tissues; synthesis of cDNA was initiated from the
XX 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
XX untranslated sequence is unique to a particular mRNA species, almost
XX all the 3'-oriented cDNAs hybridize with specific mRNAs. Each library
XX is constructed so as to reflect accurately the relative abundance of
XX different mRNAs in the particular tissue from which it was derived.
XX The appearance frequency of a given GS in a cDNA library can be
XX determined (esp. using primers and probes derived from the GS
XX sequences) as a means of diagnosing abnormal cell function or for
XX recognising different cell types.
XX
XX Sequence 82 BP; 31 A; 7 C; 14 G; 30 T; 0 other;
XX
XX Query Match 0.5%; Score 17; DB 16; Length 82;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 2521 TCTGTAAGGTTTGG 2537
DB 7 TCTGTAAGGTTTGG 23

```

RESULT 15

AAT41135

ID AAT41135 standard; DNA; 24 BP.

XX

AC AAT41135;

XX

DT 03-DEC-1996 (first entry)

XX

DE Human gene signature HUMGS01570-derived sense primer.

XX

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;

KW human; cloning; mapping; non-biased library; diagnosis; detection;

KW cell typing; abnormal cell function; primer; PCR; amplification;

KW polymerase chain reaction; ss.

XX

OS Synthetic.

XX

PN WO9514772-A1.

XX

PD 01-JUN-1995.

XX

PE 11-NOV-1994; 94WO-JP01916.

XX

PR 12-NOV-1993; 93JP-0355504.

XX

PA (MATSU) MATSUBARA K.

PA (OKUBO) OKUBO K.

XX

PI Matsubara K, Okubo K;

XX

DR WPI; 1995-206931/27.

XX

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.

PT for diagnosis of abnormal cell function, by preparing cDNA that

PT reflects relative abundance of corresp. mRNA in specific human

PT tissues

```

XX
XX Example 7; Fig 7; 2245pp; Japanese.
XX
XX PS Primers T41001-T41382 are derived from novel human gene signature (GS)
XX sequences which did not match with sequences deposited in Genbank release
XX 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
XX libraries prepared from various human tissues; synthesis of cDNA was
XX initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
XX Each library is constructed so as to reflect accurately the relative
XX abundance of different mRNAs in the particular tissue from which it was
XX derived. The appearance frequency of a given GS in a cDNA library can be
XX determined (esp. using primers and probes derived from the GS sequences)
XX as a means of diagnosing abnormal cell function or for recognising
XX different cell types. The primers T41135-6 amplify clone pm2810 which
XX comprises the GS HUMGS001570 (T20570), located on chromosome 11.
XX
XX SQ Sequence 24 BP; 6 A; 1 C; 6 G; 11 T; 0 other;
XX
XX Query Match 0.4%; Score 16; DB 16; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 2522 CTGTAAGGTTTGG 2537
DB 1 CTGTAAGGTTTGG 16

```

Search completed: January 11, 2003, 03:27:17

Job time : 719 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:52:33 ; Search time 9356 Seconds  
(without alignments)  
11549.671 Million cell updates/sec

Title: US-10-003-354-3

Perfect score: 3713

Sequence: 1 attaacagcgctggttagg.....aaacttaatgattatta 3713

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapept 60.0

Searched: 2054640 segs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*\*  
1: gb\_da:\*\*  
2: gb\_hlg:\*\*  
3: gb\_in:\*\*  
4: gb\_cm:\*\*  
5: gb\_ov:\*\*  
6: gb\_pat:\*\*  
7: gb\_ph:\*\*  
8: gb\_pl:\*\*  
9: gb\_pr:\*\*  
10: gb\_ro:\*\*  
11: gb\_sts:\*\*  
12: gb\_sy:\*\*  
13: gb\_un:\*\*  
14: gb\_vl:\*\*  
15: em\_ba:\*\*  
16: em\_fun:\*\*  
17: em\_hum:\*\*  
18: em\_in:\*\*  
19: em\_mu:\*\*  
20: em\_om:\*\*  
21: em\_or:\*\*  
22: em\_ov:\*\*  
23: em\_pat:\*\*  
24: em\_ph:\*\*  
25: em\_pl:\*\*  
26: em\_ro:\*\*  
27: em\_sts:\*\*  
28: em\_un:\*\*  
29: em\_vl:\*\*  
30: em\_hlg\_hum:\*\*  
31: em\_hlg\_inv:\*\*  
32: em\_hlg\_other:\*\*  
33: em\_hlg\_mus:\*\*  
34: em\_hlg\_pln:\*\*  
35: em\_hlg\_rnd:\*\*  
36: em\_hlg\_mam:\*\*  
37: em\_hlg\_vrl:\*\*  
38: em\_sy:\*\*  
39: em\_hlgo\_hum:\*\*  
40: em\_hlgo\_mus:\*\*  
41: em\_hlgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID

Result No.	Score	Query Match	Length	DB ID	Description
1	20	0.5	83	9	HUMSPALTC
2	19	0.5	50	6	AX165819
3	18	0.5	51	6	AX118541
4	17	0.5	25	6	AX042894
5	17	0.5	42	6	AX3509
6	17	0.5	48	6	AX3513
7	17	0.5	48	6	AX3514
8	17	0.5	51	6	AX116989
9	17	0.5	54	6	AX138031
10	17	0.5	54	6	AX14881
11	17	0.5	65	6	AX482998
12	16	0.4	24	6	E25576
13	16	0.4	25	6	AX042974
14	16	0.4	25	6	AX043091
15	16	0.4	28	6	AX73896
16	16	0.4	32	6	AX037332
17	16	0.4	51	6	AX157358
18	16	0.4	64	10	RATANSARD
19	16	0.4	65	6	AX486185
20	16	0.4	65	6	AX486614
21	16	0.4	74	6	E25575
22	16	0.4	97	6	AR014618
23	16	0.4	97	6	BD010410
24	16	0.4	97	6	I26751
25	16	0.4	98	9	HUMNTCORF4
26	16	0.4	17	6	AX216771
27	15	0.4	18	6	AX7837
28	15	0.4	18	6	AR092040
29	15	0.4	18	6	AR112175
30	15	0.4	18	6	AR149217
31	15	0.4	18	6	AX428715
32	15	0.4	19	6	AR082444
33	15	0.4	19	6	AR139000
34	15	0.4	19	6	AX039816
35	15	0.4	20	6	AX296645
36	15	0.4	22	6	I46655
37	15	0.4	24	6	AX292012
38	15	0.4	24	6	AX377075
39	15	0.4	24	6	AX444522
40	15	0.4	25	6	AX135862
41	15	0.4	26	6	AX038118
42	15	0.4	26	6	AX038119
43	15	0.4	27	6	AX286269
44	15	0.4	27	6	E09727
45	15	0.4	27	6	E09727

#### ALIGNMENTS

RESULT 1  
HUMSPALTC/c 83 bp mRNA linear PRI 13-FEB-2002  
LOCUS  
DEFINITION Homo sapiens nuclear autoantigen mRNA, partial cds; alternatively  
spliced.  
ACCESSION L79986  
VERSION L79986.1 GI:18653899  
KEYWORDS Spi100; alternative splicing; interferon-inducible protein; nuclear  
autoantigen.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE  
1 (bases 1 to 83)  
Szostekl,C., Guldner,H.H., Netter,H.J. and Will,H.

QY	DB	Matches	Best Local Similarity	Conservative	Pred. No. 1.6e+02;	Mismatches	Indels	Gaps
2567	8	19	100.0%	0	0	0	0	0
<p>RESULT 3</p> <p>AX118541 51 bp DNA Linear PAT 11-MAY-2000</p> <p>LOCUS AX118541</p> <p>DEFINITION Sequence 3664 from Patent WO0129262.</p> <p>ACCESSION AX118541</p> <p>VERSION AX118541.1 GI:14035492</p> <p>KEYWORDS human.</p> <p>SOURCE Homo sapiens</p> <p>ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.</p> <p>REFERENCE 1 (bases 1 to 51)</p> <p>AUTHORS Picoult-Newburg, L. and Pohl, M.</p> <p>TITLE Genotyping reagents, kits and methods of use thereof</p> <p>JOURNAL Patent: WO 0129262-A 3664 26-APR-2001;</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..51</p> <p>source /organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p>								
BASE COUNT	5 a	15 c	8 g	23 t				
ORIGIN								
Query Match	0.5%;	Score 18;	DB 6;	Length 51;				
Best Local Similarity	100.0%;	Pred. No. 6.2e+02;						
Matches	18;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
QY	2567	19	100.0%	0	0	0	0	0
DB	34	19	100.0%	0	0	0	0	0
<p>RESULT 4</p> <p>AX042894 25 bp DNA Linear PAT 23-NOV-2000</p> <p>LOCUS AX042894</p> <p>DEFINITION Sequence 460 from Patent WO0065088.</p> <p>ACCESSION AX042894</p> <p>VERSION AX042894.1 GI:11341502</p> <p>KEYWORDS</p> <p>SOURCE synthetic construct.</p> <p>ORGANISM synthetic construct.</p> <p>REFERENCE 1 (bases 1 to 25)</p> <p>AUTHORS Ulfendahl, P. J. and Wong, K. C.</p> <p>TITLE Primers for identifying typing or classifying nucleic acids</p> <p>JOURNAL Patent: WO 0065088-A 460 02-NOV-2000;</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..25</p> <p>source /organism="synthetic construct"</p> <p>/db_xref="taxon:32630"</p> <p>/note="HLA-C Homozygote Primer Sequence"</p>								
BASE COUNT	1 a	5 c	2 g	17 t				
ORIGIN								
Query Match	0.5%;	Score 17;	DB 6;	Length 25;				
Best Local Similarity	100.0%;	Pred. No. 2.5e+03;						
Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
QY	2999	17	100.0%	0	0	0	0	0
DB	6	17	100.0%	0	0	0	0	0
<p>RESULT 5</p>								



A93509/c 42 bp DNA linear PAT 22-JAN-2000  
LOCUS A93509  
DEFINITION Sequence 2 from Patent WO9740163.  
ACCESSION A93509  
VERSION A93509.1 GI:6741728  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Colpan,M. and Schorr,J.  
TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
JOURNAL Patent: WO 9740163-A 2 30-OCT-1997;  
COLPAN MERIN (DE); SCHORR JOACHIM (DE)  
LOCATION/Qualifiers  
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Query Match 0.5%; Score 17; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2562 CCAGCTTCTCTCTCT 2578  
|||||  
Db 41 CCAGCTTCTCTCTCT 25

RESULT 6 48 bp DNA linear PAT 22-JAN-2000  
LOCUS A93513  
DEFINITION Sequence 6 from Patent WO9740163.  
ACCESSION A93513  
VERSION A93513.1 GI:6741732  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Colpan,M. and Schorr,J.  
TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
JOURNAL Patent: WO 9740163-A 6 30-OCT-1997;  
COLPAN MERIN (DE); SCHORR JOACHIM (DE)  
LOCATION/Qualifiers  
FEATURES  
source 1..48  
/organism="unidentified"  
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BASE COUNT 19 a 11 c 9 g 9 t  
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Query Match 0.5%; Score 17; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2562 CCAGCTTCTCTCTCT 2578  
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Db 47 CCAGCTTCTCTCTCT 31

RESULT 7 48 bp DNA linear PAT 22-JAN-2000  
LOCUS A93514  
DEFINITION Sequence 7 from Patent WO9740163.  
ACCESSION A93514  
VERSION A93514.1 GI:6741733  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Colpan,M. and Schorr,J.

TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
JOURNAL Patent: WO 9740163-A 7 30-OCT-1997;  
COLPAN MERIN (DE); SCHORR JOACHIM (DE)  
LOCATION/Qualifiers  
FEATURES  
source 1..48  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 8 a 10 c 12 g 18 t  
ORIGIN  
Query Match 0.5%; Score 17; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2562 CCAGCTTCTCTCTCT 2578  
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Db 6 CCAGCTTCTCTCTCT 22

RESULT 8 51 bp DNA linear PAT 11-MAY-2001  
LOCUS AX116989/c  
DEFINITION Sequence 2112 from Patent WO0129262.  
ACCESSION AX116989  
VERSION AX116989.1 GI:14033931  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 2112 26-APR-2001;  
Orchid Biosciences, Inc. (US)  
LOCATION/Qualifiers  
FEATURES  
source 1..51  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 20 a 9 c 7 g 15 t  
ORIGIN  
Query Match 0.5%; Score 17; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2577 TTTTCTTTCTGAAA 2593  
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Db 19 TTTTCTTTCTGAAA 3

RESULT 9 54 bp DNA linear PAT 13-MAY-1997  
LOCUS I38031  
DEFINITION Sequence 1044 from patent US 5612215.  
ACCESSION I38031  
VERSION I38031.1 GI:2086021  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and  
Stinchcomb,D.T.  
TITLE Stromelysin targeted ribozymes  
JOURNAL Patent: US 5612215-A 1044 18-MAR-1997;  
LOCATION/Qualifiers  
FEATURES  
source 1..54  
/organism="unknown"  
BASE COUNT 18 a 9 c 18 g 9 t  
ORIGIN  
Query Match 0.5%; Score 17; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3286 TCAGGGGAGAGAGGGG 3302  
|||||

Db 1 TCAGGGGAGAGAGGGG 17

## RESULT 10

LOCUS 194881 54 bp DNA linear PAT 01-DEC-1998  
DEFINITION Sequence 1044 from patent US 5731295.  
ACCESSION 194881  
VERSION 194881.1 GI:3939351  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 54)  
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and  
Stinchcomb,D.T.

TITLE Method of reducing streptomycin RNA via ribozymes  
JOURNAL Patent: US 5731295-A 1044 24-MAR-1998;  
FEATURES  
LOCATION/Qualifiers  
SOURCE 1. .54  
/organism="unknown"

BASE COUNT 18 a 9 c 18 g 9 t  
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3286 TCAGGGGAGAGAGGGG 3302  
|||||

Db 1 TCAGGGGAGAGAGGGG 17

## RESULT 11

LOCUS AX482998 65 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 298 from Patent WO02053728.  
ACCESSION AX482998  
VERSION AX482998.1 GI:22317418  
KEYWORDS  
SOURCE Candida albicans.  
ORGANISM Candida albicans.  
Eukaryota; Fungi; Ascomycota; Saccharomycetalia; Saccharomycetes;  
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1  
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.  
TITLE Gene disruption methodologies for drug target discovery  
JOURNAL Patent: WO 02053728-A 298 11-JUL-2002;  
Biltra Pharmaceuticals, Inc. (US)

FEATURES  
LOCATION/Qualifiers  
SOURCE 1. .65  
/organism="Candida albicans"  
/db\_xref="taxon:5476"

BASE COUNT 17 a 8 c 9 g 31 t  
ORIGIN

Query Match 0.5%; Score 17; DB 6; Length 65;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2567 TTCCTCTCTCTTTT 2583  
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Db 2 TTCCTCTCTCTTTT 18

## RESULT 12

LOCUS E25574 24 bp RNA linear PAT 18-JUN-2001  
BASE COUNT 12 a 0 c 12 g 0 t  
ORIGIN

DEFINITION RNA molecule inhibiting hepatitis C virus NS3 protease.  
ACCESSION E25574  
VERSION E25574.1 GI:13024840  
KEYWORDS JP 1999137252-A/6.  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Satoshi,N., Pemmeccha,K. and Kotaro,F.  
TITLE RNA molecule inhibiting hepatitis C virus NS3 protease  
JOURNAL Patent: JP 1999137252-A 6 25-MAY-1999;  
AGENCY OF IND SCIENCE & TECHNOL

COMMENT OS Unidentified  
PN JP 1999137252-A/6  
PD 25-MAY-1999  
PE 07-NOV-1997 JP 1997305344  
PR

P1 SATOSHI NISHIKAWA,PEMMECCHA KUMARU,KOTARO FUKUDA PC  
C12N15/09,A61K31/70,A61K31/70,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1. .24  
/organism="unidentified".  
LOCATION/Qualifiers  
SOURCE 1. .24  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 0 a 12 c 0 g 12 t  
ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TCCTCTCTCTCTTC 2232  
|||||

Db 8 TCCTCTCTCTCTTC 23

RESULT 13  
LOCUS E25576/c 24 bp DNA linear PAT 18-JUN-2001  
DEFINITION RNA molecule inhibiting hepatitis C virus NS3 protease.  
ACCESSION E25576  
VERSION E25576.1 GI:13024842  
KEYWORDS JP 1999137252-A/8.  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Satoshi,N., Pemmeccha,K. and Kotaro,F.  
TITLE RNA molecule inhibiting hepatitis C virus NS3 protease  
JOURNAL Patent: JP 1999137252-A 8 25-MAY-1999;  
AGENCY OF IND SCIENCE & TECHNOL

COMMENT OS Unidentified  
PN JP 1999137252-A/8  
PD 25-MAY-1999  
PE 07-NOV-1997 JP 1997305344  
PR

P1 SATOSHI NISHIKAWA,PEMMECCHA KUMARU,KOTARO FUKUDA PC  
C12N15/09,A61K31/70,A61K31/70,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
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FT source 1. .24  
/organism="unidentified".  
LOCATION/Qualifiers  
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/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 12 a 0 c 12 g 0 t  
ORIGIN

Search completed: January 11, 2003, 06:03:29

Job time : 9360 secs

Query Match 0.4%; Score 16; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2217 TCTCTCCTCTCTCTC 2232  
 DB 17 TCTCTCCTCTCTCTC 2

RESULT 14  
 AX042974  
 LOCUS AX042974 25 bp DNA linear PAT 23-NOV-2000  
 DEFINITION Sequence 540 from Patent WO0065088.  
 ACCESSION AX042974  
 VERSION AX042974.1 GI:11341582  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REFERENCE  
 AUTHORS Ulendahl, P.J. and Wong, K.C.  
 TITLE Primers for identifying typing or classifying nucleic acids  
 JOURNAL Patent: WO 0065088-A 540 02-NOV-2000;  
 Amersham Pharmacia Biotech AB (SE)  
 FEATURES  
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 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 4 a 2 c 5 g 14 t  
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 Query Match 0.4%; Score 16; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2577 TTTTCTTTCTGAAA 2592  
 DB 3 TTTTCTTTCTGAAA 18

RESULT 15  
 AX043091  
 LOCUS AX043091 25 bp DNA linear PAT 23-NOV-2000  
 DEFINITION Sequence 657 from Patent WO0065088.  
 ACCESSION AX043091  
 VERSION AX043091.1 GI:11341699  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REFERENCE  
 AUTHORS Ulendahl, P.J. and Wong, K.C.  
 TITLE Primers for identifying typing or classifying nucleic acids  
 JOURNAL Patent: WO 0065088-A 657 02-NOV-2000;  
 Amersham Pharmacia Biotech AB (SE)  
 FEATURES  
 source 1..25  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 2 a 5 c 2 g 16 t  
 ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 TTTTCTTCAGATGT 83  
 DB 4 TTTTCTTCAGATGT 19

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